STIC-Biotech/ChemLib

173647

From:

Shaw, Amanda Marie

Sent: To: Wednesday, December 07, 2005 11:54 AM

STIC-Biotech/ChemLib

Subject:

sequence search for 10/713/137

Please search:

1) SEQ ID NO: 2 and 3 (each of these sequences is 24 nucleotides in length). Please limit the search results to nucleic acids that are of a length of 50 nucleotides or less.

2) SEQ ID NO: 1 (258 nucleotides in length)

The CRF has been entered:

http://expoweb1:8001/cgi-bin/expo/BioInfo/bioquery.pl?APPL_ID=10713137

Please provide a printout of the first 40 results.

Thank you,

Amanda Shaw Patent Examiner Art Unit 1634 Remsen 2E78 Mailbox: REM 2C70 571-272-8668 CREV

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

Ty	pe of Search
NA#	AA#:
S/L:	Oligomer:
Encode/	Fransl:
Structure	#:Text:
Inventor	Litigation:

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Human induc

161175 HUMINOSA A39980 AR380862 HSINOSA CQ723665 AY046510 AX067222 AF068236

4145 4145 4164 4164 4467 35764 4150 179504

115516 Sequence 1
16.115 Sequence 1
16.09210 Homo aspien
A39980 Sequence 1
AR380862 Sequence 1
A73029 H. sapiens m
CQ723665 Sequence
A7065210 Adenovira
A705294 Covis arie
BV410321 S2299690F
US9390 Sus scrofa
AF427516 Mus muscu
AF223945 Wus scrofa
AF427516 Mus muscu
AL522185 Mouse DNA
AC036147 Mus muscu
AL522185 Mouse DNA
AC036147 Mus muscu
AL522186 Cavis no
AC105495 Rattus no
AC106421 Rattus no
AC11866 Rattus nor
AY211532 Rattus nor
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BV410321 SSU59390 AF427516 AL592185

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46.0 4150 46.0 4150 49.0 1950 49.8 2838 38.8 648 38.3 178443 38.1 11006 38.1 11006 38.1 124020 38.1 124020 38.1 3974 36.7 3444 36.7 3444

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AC130289 Homo sapi
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CS101221 Sequence
X85766 H. sapiens N
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Copyright (c) 1993 - 2005 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
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ALIGNMENTS

AC036147 RN0230468 AC105495_0 AC103040 AC106421 AF027180 AY297461 RATINGSA AY211532 AY211532

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Locus	D0060518 47/58 bp DNA 11near PKI 23-7005
DEFINITION	Homo sapiens nitric oxide synthase ZA (inducible, nepatocytes)
	(NOS2A) gene, complete cds.
ACCESSION	
VERSION	DQ060518.1 GI:66268800
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
	Hominidae; Homo.
REFERENCE	1 (bases 1 to 47758)
AUTHORS	Livingston, R.J., Rieder, M.J., Shaffer, T., Bertucci, C., Baier, C.N.,
	Rajkumar, N., Willa, H.T., Daniels, M., Downing, T.K., Stanaway, I.B.,
	Nquyen, C.P., Gildersleeve, H., Cassidy, C.M., Johnson, E.J.,
	Swanson, J. E., McFarland, I., Yool, B., Park, C. and Nickerson, D.A.
 TITLE	Direct Submission
JOURNAL	Submitted (13-MAY-2005) Genome Sciences, University of Washington,
	1705 NE Pacific, Seattle, WA 98195, USA
COMMENT	To cite this work please use: NIEHS-SNPs, Environmental Genome
	Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA
	(URL: http://egp.gs.washington.edu).
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Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, P., Vo, H., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Direct Submission
                                                                                                                                                  Submitted (20-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: Plasmid; n/a; 100% of reads
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consenus quality: 111511 bases at least Q30
Consenus quality: 114471 bases at least Q20
Insert size: 185000; agarose-fp
Insert size: 115026; sum-of-contigs
Quality coverage: 15.7 in Q20 bases; sum-of-contigs
Quality coverage: 24.8 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of il consigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between a sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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0: contig of 2703 bp in length
0: gap of 100 bp
6: contig of 2076 bp in length
5: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: 127556
Center clone name: 1145_F_2
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44060: contig of 17066 bp in length
44160: gap of 100 bp
116026: contig of 71866 bp in length.
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26894: contig of 12028 bp in length
26994: gap of 100 bp
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/clone lib="RPC1-11 Human Male BAC"
1. .1896
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Web site: http://www-seq.wi.mit.edu
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clone_end:SP6
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Homo sapiens chromosome 17 clone RP11-1145F2 map 17, WORKING DRAFT
SEQUENCE, 11 unordered pieces.
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ACI31306.1 GI:22325231
HTG; HTGS_PHASE1; HTGS_PRAFT; HTGS_FULLTOP.
HOMO sapiens (human)
HOMO sapiens
HOMO sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Homo sapiens chromosome 17, clone RP11-1145F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.3e-49;
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Best Local Similarity 99.6%; Pred. No. 2.3e
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Direct Submisted (19-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 1 (bases 1 to 116599)

EBITEAN, Basisten, V. Badom, T. Bogogalavky, L. Boukhgalter, B. Cook, A. Cooke, P. DeArellano, K. Dewar, K. Diaz, J. S. Dodge, S., Farreira, P. Chang, J., Maclean, J., Machen, R., Minch, R., Liu, G., Maclean, J., Machen, R., Maid, J., Matthews, C., McCarthy, T., Wylor, J., Worli, D., Oliver, J., Matthews, C., McCarthy, T., Wylor, J., Novil, D., Oliver, J., Norman, C.H., O'Connor, T., Popter, J., Norman, J., Rowa, J., Roy, A., Schauer, S., Schubback, R., Saman, S., Severy, P., Santh, C., Spencer, B., Stonger-Thomann, N., Savery, P., Santh, C., Spencer, B., Stonger-Thomann, N., Stong, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission

AL Submitted (15-AJA-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

A (bases I to 116599) Street, Cambridge, MA 02141, USA

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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
                                                                                           Hominidae, Homo.
1 (bases 1 to 136599)
Birren, B., Nusbaum, C. and Lander, B.
Homo sapiens chromosome 17, clone RP1-66C13
                                                                                                                                                                                 Unpublished
2 (bases 1 to 136599)
                            ORGANISM
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AUTHORS
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Best Local Similarity 99.6
Matches 257; Conservative
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셤 ઠે 셤 ð 요 AC130289 136599 bp DNA linear PRI 23-JAN-2003 Homo sapiens chromosome 17, clone RPI-66C13, complete sequence. AC130289.11 GI:27877275

DEFINITION ACCESSION VERSION AC130289/c

LOCUS

KEYWORDS

241

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61 GGCTACCAGATGCCAGATGGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG
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99.6%; Pred. No. 1.9e-49;
Mismatches 0;
                                                                                                                                                                                                                                                                    / Typ. family="HERN9"

complement (25467...25477)

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complement (25494...25499)

/ note="<30 qual SNGL region"

complement (25543...25551)

/ note="<30 qual SNGL region"

2743...27546

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27548

/ rpt family="LTR12B"

27548

/ rpt family="LTR12B"
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complement (29717. .30006)
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complement (30190. .30319)
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complement(18348, .18637)
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270. 24554
270. 2451
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complement(24912. 25156)
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25157. 27242
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/9228. .20196
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17630. .17836
/rpt_family="L2"
17849. .18163
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/rpt_family="L2"
complement(28165.
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bOnly the first 136.6 kilobases of this clone are being submitted.
The remainder overlaps accession number AC005697 (WICGR project
L418).
                                                                                                                                   Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Center project name: L27646
Center project name: 66_C_13
                                                                                                                                                                                                                                                                                                                                                                                  / "ap--"RP1-66C13"
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complement(1. 1738)
/rpt_family="HERVR11"
complement(1739. 2597)
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complement(13628, .13920)
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/rrr f=-14637
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16018. 16074
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2249. 12275
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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complement (11241, 11394)
rpt family="Tigger8"
complement (11559, 11864)
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complement (9883. .10013)
rpt family="AluSq"
1199. .11219
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12617. .12907
/rpt_family="AluJb"
complement(13202. .13
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Gaps

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Pasha, A.Q. and Ahsan, A.
Method of detecting predisposition to high altitude pulmonary edema
Patent: WO 2005047540-A 1 26-MAY-2005;
Council of Scientific and Industrial Research (IN)
Location/Qualifiers
                                       PAT 10-JUN-2005
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Homo sapiens (human)

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.
                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Molecular cloning and structural organization of the human inducible nitric oxide synthese gene (NOS2)
Biochem. Biophys. Res. Commun. 219 (3), 784-788 (1996)
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                                     CS101221 259 bp DN
Sequence 1 from Patent WO2005047540.
CS101221
CS101221.1 GI:67509718
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/organism="Homo sapiens"
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H.sapiens NOS2 gene, exon 8 and 9.
X85766
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                                                                                                                                              Homo sapiens (human)
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Xu, W.
                                                                                                                                                                                                                               Hominidae; Homo.
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                                                                               HS66C13 156907 bp DNA linear PRI 17-JUN-2001 Homo sapiens chromosome 17 from PAC RPCI-1 66C13 map 17p11.2 region D178842-D17S953, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (28-APR-2000) MOLGENR, Abt Lehrach, Max Planck Institut
Submitted (28-APR-2000) MOLGENR, Abt Lehrach, Max Planck Institut
Puer Molekulare Genetik, Ihnestrasse 73, Berlin, 14195 Germany
On Jun 19, 2001 this sequence version replaced gi:13752107.
Clone received from the Resource Centre of the Human Genome Project
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/clone="PAC RPCI-1 66Cl3"
/clone=lb="RPCI1,3-5 Human PAC library, originating
insitute: Roswell Park Cancer Institute, creator: Pieter
de Jong, P. Ioannou"
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Steffens,C., Klein,M., Heitmann,K., Schuelzchen,S., Starke,A.,
Thompson,C., Radelof,U., Francis,F., Seranski,P., Poustka,A.,
Lehrach,H. and Reinhardt,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="region between markers D17S842-D17S953"
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Location/Qualifiers
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156907
/note="T7_end:PAC RPCI-1 66C13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .156907
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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AL354047.6 GI:14488115
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Hominidae, Homo.

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Hominidae, Homo.

Hominidae, Homo.

Hominidae, Homo.

Homosapicus to 1152)

Homosapicus finhibitors of inducible nitrogen oxide synthetase activation

Patent: WO 0166791-A 2 13-SEP-2001;

FUJISMAM PHARMACEUTICAL CO LTD, YOSHINORI ISHII, YOSHIKO UEDA, MORITA IWAMI, HIROYUK ARAKAWA, YOSHITADA NOTSU

OS Homo sapiens (human)

PN WO 0166791-A/2

PN HOMA-2001 WO 2001JP001865

PR 10-MAR-2000 JP 00P 72480

PR 10-MAR-2000 JP 00P 72480

PN WO 115MII, YOSHIKO UEDA, MORITA IWAMI, HIROYUKI ARAKAWA, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Method for screening of inhibitors of inducible nitrogen oxide synthetase activation.
Submitted (02-MAY-2001) Departamento de Bioquimica, Universidade de Sao Paulo, Rua Professor Lineu Prestes, 748/bloco 12/sala 1200, Sao Paulo, SP 05508-900, Brazil
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 ACTCAGGTACCCGGCCCAGCCTCAGCCRCGGCCATTGGGGCGGGGGCCCCGTGGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 CGAGTGACAGAGCCCACAGGAGACACGCAGCCCGGGCTTACAGACTCACAGGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /produčt="nitiric oxide synthase 2A"
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/chromosome="14"
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C1201/25,C12N15/52,G01N33/50,G01N33/15
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                                                                              Location/Qualifiers
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BD097464.1 GI:22643038
WO 0166791-A/2.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                  .>66
/gene="NOS2A"
/codon_start=1
                                                                                                                                                                                                                                                                                           /gene="NOS2A"
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                                                                                                                                                                                                                                                                   <1. .>257
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Ateles belzebuth chamek
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammala; Eutheria; Euarchontoglires; Primates; Platyrrhini;
Cebidae; Atelinae; Ateles.
1 (bases 1 to 257)
Seuanez,H.N., Lima,C.R., Lemos,B., Bonvicino,C.R., Moreira,M.A. and
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Gene assignment in Ateles paniscus chamek (Platyrrhini, Primates).
Allocation of 18 markers of human syntenic groups 1, 2, 7, 14, 15,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 602;
                                                                                                                                                                                                                                                                                                                                            /gene="NOS2"
137. .278
/gene="NOS2"
/product="inducible nitric oxidase synthase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="NOS2"
/product="inducible nitric oxidase synthase"
/number=9
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                                                                                 /ustrate in the property of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 236.8; DB 8;
Pred. No. 2.7e-44;
1; Mismatches 13;
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                                             L. .602
/organism="Homo sapiens"
             Location/Qualifiers
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llarity 94.6%;
Conservative 1
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 244; Conserv
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/protein_id="AAA36375.1"
/bx xref="c1:404049"
/tanslation="MACPWERFRYREHQYAMNGEKDINNNVEKAPCATSSPVTQDDL/translation="MACPWERFRYREHQYAMNGEKDINNNVEKAPCATSSPVTQDDLQYHNLSKQQNESPQPLYETGKKSPESIVKLDATPLSSPRHYALKNWGSGMTFQDTLHHKAKGILTCRSKSCLGSIMTPKSLTRGPRDKPTPPDELLPQAIEFVNQYYGSFKEAKIE
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TAREMFEHICRHYRYSTNNGNIRSALTVFPQRSDGKHDFRWNAQLIRYAGYQMPDGS
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KYGDPANVEFTQLCIDLGWKEKYGRPOVPLVLAGNGNGNFETETRPFDLULEVAMEHP
KYGRELELKWYALPAVANMLLEVGGLEFPGCPFRGWYMGTEIGYRDFCDVQRYNI
EEVGRRWGLETHKLAGAVANMLLEVGGLEFPGCPFRGWYMGTEIGYRDFCDVQRYNI
EEVGRRWGLETHKLADALWCDQAVVENIAVHSFQKONVTIMDHHSAAESFMKYMQU
YRSRGGCPADWIMLVPPMSGSITPVFHQEMLNYVLSPFYYYQVEAWKTHVWQDEKRRP
FKYRGTFATKLSCLEERRLLLYATRSRVRYTIFATETGKSALAWUGALFSCAFN
GLGSSWYRFRCARFANDLOKLSHJGASQLTPWGEGDELSGGEDAFRSWAVQFFKAACE
TFDVRGKQHIQIPKLYTSNVTWDPHHYRLVQDSQPLDLSKALSSWHARNVFTWRLKSR
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QYTWILEALDESGSYWYSDKRLPPCLSQALYFLDITTPPFULLQKAQVATEBER
QRLEALCQPSSYSKWKTNEPTELSUZEFPSIRVSAGFLLSQLPILKPRFYSISSSR
DHTPTEIHLTVAVYTYHTRDGQGPLHHGVCSTWLNSLKPQDPVPCFVRNASGFHLED
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EMAQKGVLHAVHTAYSRLPGKPKVYVQDILRQQLASEVLRVLHKEPGHLYVCGDVRMA
RDVAHTLKQLVAAKLKLNEEQVEDYFFQLKSQKRYHEDIFGAVFPYEAKKDRVAVQPS
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Homo sapiens inducible nitric oxide synthase mRNA, complete cds.
                                                                                                                                                                                        61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                   745 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                               1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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1 (bases 1 to 3595)
Sherman,P.A., Laubach,V.E., Reep,B.R. and Wood,E.R.
Purification and CDNA sequence of an inducible nitric oxide synthase from a human tumour cell line
Biochemistry (1993) In press
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       Length 3462;
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/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="texon:9606"
/db xref="texon:9606"
/cbll_line="DLD-1"
/tissue_type="colorectal adenocarcinoma"
/tissue_lib="ATCC cc1221"
Score 120.4; DB 6;
Pred. No. 1.2e-17;
0; Mismatches 1;
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/note="inducible"
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nitric oxide synthase.
Homo sapiens (human)
Homo sapiens
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46.7%;
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Best Local Similarity 99.2
Matches 121; Conservative
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1 (bases 1 to 3462)

1 shii, Y., Ueda, Y., Lwami, M., Arakawa, H. and Not, Y.

1 shii, Y., Ueda, Y., Uami, M., Arakawa, H. and Not, Y.

1 shii, Y., Ueda, Y., I shiibitors of inducible nitrogen oxide synthetase activation

1 satent: WO 0166791 al. 35EP-2001, Patent: WO 0166791 al. A. 1 13-5EP-2001, PATENTA PHARMACEUTICAL CO LTD, YOSHINORI ISHII, YOSHIKO UEDA, MORITA IWAMI, HIROYUKI ARAKAMA, YOSHITADA NOTSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3462 bp DNA linear PAT 27-AUG-2002 Method for screening of inhibitors of inducible nitrogen oxide spans.
    Method for screening of inhibitors of inducible nitrogen oxide
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R 10-MAR-2000 JP 00P 72480
I YOSHINORI ISHII, YOSHIKO UEDA, MORITA IWAMI, HIROYUKI ARAKAWA, PI
YOSHITADA NOTSU
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Method for screening of inhibitors of inducible nitrogen oxide
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                               1. .1152 / Location/Qualifiers (human)'.

Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Human inducible nitric oxide synthase mRNA, complete cds.
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Treatment of viral influenza with antisense oligonucleotides
Patent: WO 0078946-A 2 28-DEC-2000;
Eastern Virginia Medical School (US)
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Pred. No. 1.2e-17;
0; Mismatches 1;
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                         3946 bp
Sequence 2 from Patent WO0078946.
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EHLARVEAVTREI ETTTYYQLTGDELL FATKQMRARPRCIGRI OWSNLQVPGASLKE
TAREMPEHI CRHVRYTSTTYYQLTGDELL FATKQMRARPRCIGRI OWSNLQVPDARSCS
TAREMPEHI CRHVRYTSTTYYQLTGDELL FATKQMRARAPETGRI OWSNLQVPDAS
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YRRGGCPADMIWLYPPROGSITPVEHQEMLKYVLSPFYYQVRAWKTHVWQDEKRRP
KRREI PLKVLVKAVLFACMLMRKTMASRVRYTILFATETGKSEALAMIGALESCAPN
RKYCYNDKTRLBCLEBERLLLVYTSTFFGNGDCGPGNGSTGLKSSLPMLKSDLINKFRY XAVF
GLGSSBYFRFCAFAHILLVYTSTFFGNGDCGRGGGLKGSLPMLKSLINKFRY XAVF
GLGSSBYFRFCAFAHILLVYTSTFFGNGDCGGGGGLKSSPAKSWAVQTFKAACE
TFDVRGKQHIQIPKLYTSNVTWDPHYYRLVQDSQPLDLSKALSSMHAKNYFTMRLKSR
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QRLBALCQPSEYSKKFTNSPTFLEYLEEPESLWSAGAFLLSQLPILXRRFYSTSSPR
QRLPTEIHLTVAVVYTYHTROGQEPLHQVCSTWLNSLKPQDPVPCFVRNASGFHLPED
PSHPCTLIGPCTGIAPPRSFWQQRLHDSQHKGYRGGRAYLVFGCRRPDEDHIYQCERN
EMAQKGVLHAVHTAYSRLPGKPKVYYQDIIRQQLASEVLRVLHKEPGHLYYCGDVRMA
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Human inducible nitric oxide synthase mRNA, complete cds.
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/translation="MACPWKFLFKTKFHQYANNGEKGINNNVEKAPCATSSPVTQDDL
QYHNLSKQQNESPQPLVETGKKSPESLVKLDATPLSSPRHYRIKNWGSGMTFQDTLHH
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                                                                                                                 880
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California, San Diego, 9500 Gilman Drive, La Jolla, CA 92093-0663,
USA
                                                                                                                                                                        Hominidae, Homo.

1 (bases 1 to 3855)

and Lotz,M.

Bibe,G., Rediske,J. and Lotz,M.

Inducible nitric oxide synthase from human articular chondrocytes:

CDNA cloning and analysis of mRNA expression

Biochim. Biophys. Acta 1208 (1), 145-150 (1994)
                                                                                                                                                      GGCTACCAGATGCCAGATGGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                         Gaps
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Length 3595;
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/product="inducible nitric oxide synthase"
/protein_id="AAA56666.1"
                                       Indels
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.194
 Score 120.4; DB 8;
Pred. No. 1.2e-17;
0; Mismatches 1;
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="articular chor
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   Query Match
Best Local Similarity 99.2%;
Matches 121; Conservative
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U05810.1 GI:452487
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HSU05810
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EHLARVEAVTKEIETTGTYQLTGDELIFATKQAWRNAPRCIGRIQWSNLQVFDARSCS
TAREMFEHICRHVRYSTNNGNIRSAITVFPQRSDGKHDFRVWNAQLIRYAGYQMPDGS
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PSPPCILIGPGGTAPPRSFWQQRLHDSGHKGYNGGRWTLYFGGRRPBEHIYOBEML
EMAGKGYLHAVHTASRLPGRRPKVYODILRQCASBVLRVLHKEPGHLYVODVRA
RDVAHTLKQLVAAKLKLNEEQVEDYFFQLKSGKRYHEDIFGAVFPYEAKKDRVAVQPS
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QYHNLSKQQNESPQPLVETGKKSPESLVKLDATPLSSPRHVRIKNWGSGMTFQDTLHH
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Hominidae; Homo.
1 (bases 1 to 3946)
Guo,F.H., De Raeve,H.R., Rice,T.W., Stuehr,D.J., Thunnissen,F.B.
                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (20-JAN-1995) Serpil C. Erzurum, Pulmonary & Critical
Care Medicine, Cleveland Clinic Foundation, 9500 Euclid Avenue,
Cleveland, OH 44195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                  Continuous nitric oxide synthesis by inducible nitric oxide synthase in normal human airway epithelium in vivo Proc. Natl. Acad. Sci. U.S.A. 92 (17), 7809-7813 (1995)
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Pred. No. 1.2e-17;
0; Mismatches 1;
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/protein_id="AAB60366.1"
/db_xref="G1:687681"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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Erzurum, S.C.
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Best Local S
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                                                                                                                                              TITLE
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RESULT 14 HUMITONOS

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/ codon betacle
/product="inducible type of nitric oxide synthase"
/product="inducible type of nitric oxide synthase"
/protein_id="BAA05531.1"
/protein_id="BAA05531.1"
/db.xref="inducible"
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/translation="wacpwkrelrerwkehoyamvgekolrerwkehoyamsterwkehold
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/redwyalpavwgerolololowkehoyamvervekorsporperucymyarilersporpulerwhehold
/redwyalpavwalpavanmilerwehold
/redwyalpavwalpavanmilerwalpavarvileraterwehold
/redwyalpavarranswyalpavarvileraterwehold
/redwinterwehold
/redwyalpavarranswyalpavarvileraterwehold
/redwyalpavarvileraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleraterylerateryleratery
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PSHPCILIGPGTGIAPFRSFWQQRLHDSQHKGVRGGRMTLVFGCRRPDEDHIYQEBML
EMAQKGVLHAVHTAYSRLPGKRKVYYQDILRQQLASBVLRVLHKEPGHLYYCGDVRWA
RDVAHTLKQLVAAKLKLNEEQVEDYFFQLKSQKRYHEDIFGAVFPYEAKKDRVAVQPS
SLEMGAL"
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15. .347

/EC number="1.14.13.39"

/note="This human inducible NOS possessed consensus

recognition sites for the cofactors FMN, FAD and NADPH and

calmodulin recognition sites."
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PRI 04-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (18-7AN-1994) Atsushi Hokari, Jikei University School of Medicine, Tokyo, Department of Internal medicine, Division of Gastroenterclogy and Hepacology; 3-25-8 Nishishimbashi, Minato, Tokyo 105-0003, Japan (E-mall:hokari_a@jikei.ac.jp, Tel:03-3433-1111, Faz:03-3435-0569)
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1 (bases 1 to 3963)
Hokari,A., Zeniya,M. and Esumi,H.
Cloning and functional expression of human inducible nitric oxide synthase (NOS) DNA from a glioblastoma cell line A-172
J. Blochem. 116 (3), 575-581 (1994)
                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
1963 bp mRNA linear PRI 04-OCT-20 HUMITONOS HUMIA for inducible type of nitric oxide synthase, complete
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                                                                                                                                                                                                         inducible type of nitric oxide synthase; cytokine-related
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/clone_lib="lambda ZAPII"
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/db_xref="taxon:9606"
/cell_line="A-172"
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Hokari,A.
                                                                                                                                                                                                                                       Homo sapiens (human)
Homo sapiens
                                                                                                                            D26525
D26525.1 GI:559326
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Best Local Similarity 99.23
Matches 121; Conservative
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                                                                                                                   ACCESSION
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PAT 11-MAR-2004

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1 (bases 1 to 4062)
Au Young J. and Seilhamer, J.J.
Acomposition for the detection of signaling pathway gene expression
Patent: US 6500938-A 1478 31-DEC-2002;
Incyte Genomics, Inc.; Palo Alto, CA;
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Patent: EP 1394274-A 155 03-MAR-2004;
Genox Research, Inc. (JP)
Location/Qualifiers
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                               CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                              CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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Pred. No. 1.2e-17;
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Pred. No. 1.2e-17;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="unassigned DNA" /db_xref="taxon:9606"
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/organism="Homo sapiens"
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CQ776469.1 GI:45379859
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Best Local Similarity 99.2%;
Matches 121; Conservative
99.2%;
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Best Local Similarity 99.2
Matches 121; Conservative
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Patent: EP 1394274-A 38 03-MAR-2004;
Genox Research, Inc. (JP)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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                                                                                                                                                                                                                                                                              Unknown.
Unknown.
Unclassified.
1 (bases 1 to 4062)
1 (bases 1 to 4062)
Thigppn.A., Hobmeier, H.-E., Newgard, C.B., Unger, R.H.,
Shimabukuro, M., Chen, G., Rhodes, C.J., Hugl., S.R. and Cousin, S.
Methods and compositions relating to no-mediated cytotoxicity
Patent: US 6171856-A 11 09-JAN-2001;
Location/Qualifiers
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    .4062
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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Sequence 11 from patent US 6171856.
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Sequence 38 from Patent EP1394274.
CQ776352 CQ776352.1 GI:45379742
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Homo sapiens
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Matches 121; Conservative
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U31511.1 GI:951320
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QYHLLSKQONESPQPLVETGKKSPESLVKLDATPLSSPRHYRIKNSGWFFQDTLHH
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EHLARVERATWEIETTGTYQLTGDELIFATKQAWRNAPRCIGRIQWSDLARSCS
TAREMFEHICRHVRYSTNNGNIRSAITVFPQRSDGKHDFRVWNAQLIRYAGYQMPDGS
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KYBRPRELELKWYALPAVANYLLEVGGLEPECCPFNGAYMGTET GVRDPCDVQRYNIL
EEVGRRMGLETHKLAS TROQAVE III AVLHSFQKQNVTI MDHISAAESFMKYMQNE
YRSRGGCPADNI MLVPPMSGSI I PVFHQEMLAYVLSPPYYQVRAMKTHVWQDBERRP
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Park,C., Gianotti,C., Park,R. and Krishna,G.
Direct Submission
Submitted (11-JUL-1995) Chang-Shin Park, Lab. of Molecular
Immunology, NHLBI, 9000 Rockville Pike, Bethesda, MD 20892-1760,
                                                                                                                      Gapa
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1 (bases 1 to 4062)

Park, C.S., Park, R. and Krishna, G.

Constitutive expression and structural diversity of inducible isoform of nitric oxide synthase in human tissues

Life Sci. 59 (3), 219-225 (1996)
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                                                                                          Length 4062;
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                                                                                       Score 120.4; DB 6;
Pred. No. 1.2e-17;
0; Mismatches 1;
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'gene="NOS"
'note="inducible isoform"
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/chromosome="17"
                                              /mol_type="genomic DNA'
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/organism="unknown"
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GLGSSMYPRFCARABUID DOKLSHLGARQUIDPNGEGDELSGQEDAFRSMANGERTAGE
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ENAQKGVLHAVHTAYSRLFWQRLHDSQHKGVRGRNTLVFCRRPEDEDHIYQEEML
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RDVAHTLKQLVAAKLKLNEEQVEDYFFQLKSQKRYHEDIFGAVFPYBAKKDRVAAVQPS
SLEMSAL"
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1 (Dases 1 to 4145)

1 (Dases 1 to 4145)

2 Billiar,T.R., Nussler,A.K., Geller,D.A. and Simmons,R.L.

CDNA clone for human inducible nitric oxide synthase and process
for preparing same

Patent: US 5468630-A 1 21-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 4062;
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larity 99.2%; Pred. No. 1.2e-17;
Conservative 0; Mismatches 1
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1. .4145
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Sequence 1 from patent US 5468630.
                                                                                                                                                                                                                                                                                                               /gene="NOS"
/note="16 A nucleotides"
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Best Local Similarity 99.2
Matches 121; Conservative
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SHLAVEAVTEATKET
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GLGSSMYPRFCAFAHDI DQKLSHLGASQLTPWGEGDBLSGGDAFRSWAVQTFKRACF
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QTVRLEDLDSGSYWVSDKRLPPFCSLSQALTYSPDITTPPTQLLLQXLAQVATEEPER
QNLQSPFSSKWKFTNSPFFLERVBERPERLS
                                                                                                                                                                                                                                                                                                                                              DHTPTEIHLTVAVVTYHTGDGQGPLHHGVCSTWLNSIKRQDBVPCFVRNASAFHLPED
PSHPCILIGPCTGIVPFRSFWQQRLHDSQHKGVRGGRWTLVFGCRRPDEDHIYQEEML
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RDVAHTLKQLVAAKLKLNEEQVEDYFPQLKSQKRYHEDIFGAVFPYEAKKDRVAVQPS
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 4164)

1 (bases 1 to 4164)

INDUCIBLE NITRIC OXIDE SYNTHASE AND GENE THEREFOR PALENT: WO 9423038-A 1 13-OCT-1994;

WELLCOME FOUND (GB)

OTHER POLICIAN (GB)

OTHER POLICIAN (GB)

LOCATION (OBILIAN (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3669. .4145
/gene="inducible nitric oxide synthase"
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/organism="Homo sapiens"
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/cell_type="CHONDROCYTE"
226. .3687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4164 bp
Sequence 1 from Patent WO9423038.
A39980
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SOURCE
ORGANISM
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VERSION
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AUTHORS
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Homo sapiens inducible nitric oxide synthase mRNA, complete cds.
L09210
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Sluto, M., Wang, S.C., Nakayama, D.K., Simmons, R.L., Snyder, S.H. and
Billiar, T.R.
Molecular cloning and expression of inducible nitric oxide synthase
           PAT 07-0CT-1997
                                                                                                                                                                                1 (bases 1 to 4145)
Billiar, T.R., Tzeng, E., Nussler, A.K., Geller, D.A. and Simmons, R.L.
Inducible nitric oxide synthase gene for treatment of disease
Patent: US 565855-A 19-AUG-1997;
Location/Qualifiers
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Proc. Natl. Acad. Sci. U.S.A. 90 (8), 3491-3495 (1993)
7682706
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           linear
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//gene="inducible nitric oxide synthase"
207...3668
/gene="inducible nitric oxide synthase"
/function="enzyme"
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 120.4; DB 6;
Pred. No. 1.2e-17;
0; Mismatches 1;
           DNA
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Homo sapiens (human)
Homo sapiens
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           161175 4145 bp
Sequence 1 from patent US 5658565.
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/cell_type="hepatocyte"
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Best Local Similarity 99.2%;
Matches 121; Conservative (
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                                                                            GI:2479123
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                                                                                                                                                              Unclassified
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DEFINITION
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JOURNAL
                                 DEFINITION
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FEATURES
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PAT 05-MAR-1997

linear

Gaps

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Length 4145;

PRI 13-JAN-1994

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Direct Submission
Submitted (23-APR-1993) I. Charles, Wellcome Research Laboratories,
Ble. 113, Deot. of Cekk Biology, Langley Park, Beckenham, Kent, BR3
3BS, UK
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Cloning, characterization, and expression of a cDNA encoding an inducible nitric oxide synthase from the human chondrocyte Proc. Natl. Acad. Sci. U.S.A. 90 (23), 11419-11423 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                                                                                                                                                                                                                                       linear
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99.2%; Pred. No. 1.2e-17;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                     4164 bp mRNA
H.sapiens mRNA for nitric oxide synthase.
X73029
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/product="nitric oxide synthase"
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| . .4164
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Cocks B.G., Stuart, S.G. and Seilhamer, J.J.
Compositions for the detection of blood cell and immunological response gene expression
Patent: US 6607879-A 1407 19-AUG-2003;
Incyte Corporation; Palo Alto, CA
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                                                                               1030 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG 1089
                                                                                                                                                                                                                                         PAT 03-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                               Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 864
                                                               61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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    9
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Construction and characterization of a clinical grade adenoviral vector encoding the human iNOS cDNA Unpublished
2 (Dases 1 to 35764)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
    CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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Adenoviral expression vector Ad-hiNOS
Other sequences; artificial sequences; vectors.
1 (bases 1 to 35764)
Shapiro,R., Gao,W., Tzeng,E., Robbins,P.D., Timoty,B.R. and
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                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent: WO 02068579-A 9599 06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
                                                                                                                                                                                                                                Sequence 9599 from Patent W002068579.
CQ723665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                     CQ723665.1 GI:42284522
                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
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Best Local Similarity
Matches 121; Conserv
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CQ723665
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QTVRLEDLDSGGSYWYSDKRLPPCSLSQALTYSPDITTPPTQLLLQKLAQVATEEPER
QTVRLEDLOSESTSKWKTTNSPTFLEVLBEPPELKSAGAFLLSQLPILLQKRFYSISSR
DHTPTEIHLTVAVYTYTTGDGGLHHGVGTWLNSLKPQDPVPCFVRNASAFHLPED
PSHPCTLIGPGTGTTATAVAYTYTTGDGCDLHHGVGTWGGRYTLVFCGTRRDEDHIYQBENL
EMAQKGVLHAVHTAYSRLPGKPKVYVQDILRQQLASEVLRVLHKEPGHLYVCGDVRMA
RDVAHTLKQLVAAKLKLNEEQVEDYFFQLKSQKRYHEDIFGAVFPYEAKKDRVAVQPS
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/organism="Adenoviral expression vector Ad-hiNOS"

/mol type="genomic DNA"

/db xref="taxon:170404"

/note="recombinant human adenovirus type:5 encoding human

iNOS; derived from pAdLox shuttle vector and donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CAGCGGAGTGATGCCAAGCACGTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
Direct Submission
Submitted (18-JUL-2001) Surgery, University of Pittsburgh, 300
Technology Drive, Pittsburgh, PA 15219, USA
Location/Qualifiers
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46.7%; Score 120.4; DB 11; Length 35764;
Best Local Similarity 99.2%; Pred. No. 8.4e-18;
Matches 121; Conservative 0; Mismatches 1; Indels 0; (
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/note="SV40 early polyadenylation signal"
4961. .4965.
/note="SV40 polyadenylation signal"
5044. .5077
/bound_molety="LoxP"
35661. .35764
/note="terminal repeat"
/rpt_type=inverted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/produce=inducible nitric oxide synthase"
/protein_id="AAL02120.1"
/db_xref="GI:15636800"
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KEYWORDS
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AC158064/c
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1 (bases 1 to 4150)
Luss,H., Li,R.-K., Shapiro,R.A., Tzeng,E., McGowan,F.X., Yoneyama,T., Hatakayama,K., Geller,D.A., Mickle,D.A.G., Simmons,R.L. and Billiar,T.R.
Dedifferentiated human ventricular cardiac myocytes express inducible nitric oxide synthase mRNA but not protein in response to 1L-1, TNF, IFNgamma, and LPS
J. Mol. Cell. Cardiol. 29 (4), 1153-1165 (1997)
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                                                                    PAT 24-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF068236 4150 bp mRNA linear PRI 07-JUN-195
Homo sapiens inducible nitric oxide synthase (NOS) mRNA, complete
                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gape
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Treatment of Viral infiluence with antisense oligonucleotides
Patent: WO 0078846.A 3 28-DEC-2000;
Eastern Virginia Medical School (US)
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Submitted (26-MAY-1998) Pharmacology, Westf.Wilhelms-Univ.,
Domagkstr. 12, Munster D-48149, Germany
Location/Qualifiers
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Luss, H., Li,R.-K., Shapiro,R.A., Tzeng,E., McGowan,F.X.,
Yoneyama,T., Hatakayama,K., Geller,D.A., Mickle,D.A.G.,
Simmons,R.L. and Billiar,T.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 4150;
                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
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Pred. No. 2.7e-17;
0; Mismatches 2;
                                                                    DNA
                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="unassigned DNA" /db_xref="taxon:9606"
                                                             Sequence 3 from Patent WO0078946.
AX067222
                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                    AX067222.1 GI:12544879
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Best Local Similarity
Matches 120; Conserval
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AF068236
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                              RESULT 28
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RDVAHTLKQLVAAKLKLNEEQVEDY FFQLKSQKRYHEDI FGAVFPYEAKKDRVAVQPS
SLEMSAL"
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Bos taurus clone CH240-54J11, WORKING DRAFT SEQUENCE, 16 unordered
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Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
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46.0%; Score 118.8; DB 8; Length 4150;
Best Local Similarity 98.4%; Pred. No. 2.7e-17;
Matches 120; Conservative 0; Mismatches 2; Indels 0;
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ACIS8064.2 GI:68266847
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
BOB taurus (cow)
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1. 4150
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235. 3696
/gene="NOS"
/note="NOS II"
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1 (bases 1 to 179504)
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Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu

Center code: BCM

Center project name: FDEA Center clone name: CH240-54J11 ------ Summary Statistics Assembly program: Atlas 3.0;

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Direct Submissions of the Act of 
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Carter, K., Cavacos, I., Ceasar, H., Center, A., Chavez, D., Chen, Z., Chacko, J., Chavez, D., Chen, S., Chen, Y., Charez, D., Chen, S., Chen, Y., Charez, D., Chen, S., Chen, S., Chen, Y., Chen, Y., Chavez, D., Chen, S., Chen, S., Chen, Y., Chen, Y., Chen, J., Charez, D., Chen, S., Denson, S., Derano, C., Ding, Y., Dinh, H., Divya, K., Dayla, M., Darban, R., Dayla, R., Dester, M., Dagan-Rocha, S., Dunn, A., Durbin, R., Duval, R., Bavee, K., Bander, M., Gapie, M., Garta, M., Malla, M., Garta, M., Malla, M., Garta, M., Malla, M.,
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Direct Submission

Direct Submission

Of Modecular and Human Geneme Sequencing Center, Department of Modecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cow Genome Sequencing Consortium.
Direct Submission
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JOURNAL
REFERENCE
AUTHORS
TITLE
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AUTHORS
TITLE
JOURNAL
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Center: Baylor College of Medicine

COMMENT

NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. Consensus quality: 174250 bases at least Q40
Consensus quality: 175616 bases at least Q30
Consensus quality: 1756727 bases at least Q30
Estimated insert size: 174799; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation contig of 1552 bp in length
gap of 50 bp
gap of 50 bp
contig of 46345 bp in length
gap of 395 bp
contig of 44381 bp in length
gap of 50 bp
gap of 50 bp
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contig of 1060 bp in length
gap of unknown length
contig of 1060 bp in length
contig of 1060 bp in length
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gap of unknown length
contig of 1080 bp in length
gap of unknown length
gap of unknown length
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VGRRYGLETHKLASIWKDRATVEINVAVLHEFOKONTIMDHHSAAESFMKYMONEYR
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ARKGYLHEVHTAYSSLPDOSKYYYQDILRQBLAGGGRWTLVFGGGHLYWGENARD
VAHSLKQLMATALSLNEEQVEDYFFQLKNQK"
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Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
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Paired-end low-coverage whole genome shotgun reads were generated
from 9 breeds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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S229P690FE2.TO GermanShepherd Canis familiaris STS genomic,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 2838;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.8%; Score 102.8; DB 4 ilarity 90.2%; Pred. No. 1.4e-13; Conservative 0; Mismatches 12
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Fax: 6172580903
Email: kersli@genome.wi.mit.edu
Primer A: No sequence submitted
Primer B: No sequence submitted
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Ovis aries inducible nitric oxide synthase mRNA, partial cds.
AF223942
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QEMFEHICRHVRYATNNGNIRSAITVFPQRSDGKHDFRVWNAQLIRYAGYQMPDGSIR
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1 (bases 1 to 2838)

Mershon, J.L., Baker, R.S. and Clark, K.E.

Satrogen increases iNOS expression in the ovine coronary artery Am. J. Physiol. Heart Circ. Physiol. 283 (3), H1169-H1180 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
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Submitted (12-2MN-2000) Department of Obstetrics and Gynecology, University of Cincinnati Medical Center, 231 Bethesda Ave, Cincinnati, OH 45267-0526, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.0%; Score 116; DB 14; Length 179504; 89.3%; Pred. No. 6.7e-17; tive 0; Mismatches 15; Indels 0;
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/protein_id="AAF34710.1"
/db_xref="GI:6980068"
                                                                                                                                                                                                                                                                                                   /estimated_length=unknown
173901. .174000
                                                                                                                                                                                                                                                                                                                                                                         /estimated_length=unknown
175180. .175279
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178073. .178172
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172741. .172840
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    2838
    organism="Ovis aries"
/mol type="mRNA"
    db xref="taxon:9940"

125884. .125933
/estimated length=50
129690. .129739
/estimated length=50
144940. .145284
                                                                                                                                                                   /estimated_length=345
171601. .171700
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AF427516 38817 bp DNA linear ROD 29-OCT-2001
Mus musculus inducible nitric oxide synthase gene, complete cds.
AF427516
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Servier Research Institute, 125, Chemin de Ronde, Croissy sur Seine
                                                                                                                                                                                                                                                                                                                                                                       /translation="DarscstagemfehicrhlryatnngnirsaltvePqqrsDgkdd
RwnaxQliftraxdgydrptTidDpayoFtQtclDdwkrygreDvveLvLhabGR
DPBLFEIPDDLVLEVPMEHPKTEMPGBLBLKWYALPAVANMLLEVGGLEFPGGFPNGW
YMGTBIGVRDFCDVQRYNILEEVGRRMGLETHKLASLWKDRAVVEINVAVLHSFQ"
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14382. .14544,15433. .15524,16591. .16732,16830. .16969,
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Genomic structure of the murine inducible nitric oxide synthase (i-NOS) gene
Unpublished
2 (bases 1 to 38817)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
         Murtaugh, M.P., Pampusch, M.S., Harsch, S. and Bennaars, A.M. Direct Submission

Direct Submission
Submitted (27-MAY-1996) Vet. PathoBiol., Univ. of Minn., 1971
Commonwealth Ave., St. Paul, MN 55108, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coge, F., Levacher, B., Rique, H., Leopold, O., Boutin, J.A. and
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                               /cell_type="ConA, LPS stimulated splenocytes"
<1. .>647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 647;
                                                                                                                                                                                                                                                                                        /product="inducible nitric oxide synthase"
/protein_id="AAB40614.1"
/db_xref="G1:1777980"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.6%; Score 99.6; DB 4;
88.5%; Pred. No. 9.4e-13;
iive 0; Mismatches 14;
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/mol type="genomic DNA"
/strain="CD-1"
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/chromosome="11"
join(1. .25,1252. .140
                                                                                                                                                           /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
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Mus musculus
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(bases 1 to 647)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                           detection was carried out by SSAHA-SNP. 1637780 SNPs were annotated with alleles from the boxer and the poodle. The validation rate for these SNPs was estimated at approximately TBD%. Internal-WGA-discovery (I-WGA): A third set of SNPs were discovered by comparing reads in the WGA assembly. SNPs were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSUS9390 647 bp mRNA linear MAM 14-JAN-1997
Sus scrofa inducible nitric oxide synthase mRNA, partial cds.
US9330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  defined as mismatch positions that had a base quality of >= 30 on both reads in a region that aligned without gaps, and with at most one additional mismatch in the ten flanking bases. For each allele, at least one additional read had to confirm it. 731476 SNPs were annotated with alleles between the two boxer alleles. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa (pig)
Sus scrofa
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                         A second set of SNPs was generated using a similar methodology except that the contigs from the 1.5x poodle assembly (Kirkness 2003) were used instead of WGS reads. Since this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ၀
reads were placed uniquely on the CanFam1.0 boxer assembly
                                                                    485941 SNPs were annotated with alleles from the boxer and the breed or canid from which the particular was considered care approximately 98%.

WGA-discovery (WGA) of Boxer/Poodle SNPs:
                             and SNP detection was carried out by SSAHA-SNP. 863872 reads were annotated as STSs and
                                                                                                                                                                                                                                                                              sequence lacked base quality scores, arbitrary quality scores of phred 40 were assigned before the poddle sequence was placed uniquely on the CanFaml.0 becar assembly and SNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.8%; Score 100.2; DB 10; Length 648; 79.6%; Pred. No. 6.8e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
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/db_xref="taxon:9615"
/map="+ 9 22-578 34794085-34794641"
/clone_lib="GermanShepherd"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Canis familiaris"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            validation rate for these SNPs
was estimated at approximately TBD%.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTACCCGGCCCAGCCTCAGCCRCCGGC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grecadarceaectregreereac 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U59390.1 GI:1777979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 79.6
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 33
SSU59390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCUS
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regions were either double-granded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality) = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30 Mouse BAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBAACB3.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
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/db_xref="texon:10090"
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/orus tag="RP23-341J22.1-001"
/locus tag="RP33-341J22.1-001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="match: ExTa: Em:Al426142 1 Em:Al480655.1
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Em:Al59346.1 Em:Al41312.1 Em:Al480655.1
Em:BE447088.1 Em:BE447713.1 Em:BE650066.1 Em:BE85575.1
Em:BE47088.1 Em:BE47713.1 Em:BE650066.1 Em:BE85575.1
Em:BM937863.1 Em:BE47713.1 Em:EM550066.1 Em:BE85575.1
Em:BM937863.1 Em:BY479089.1 Em:BX519743.1 Em:BX535492.1
Em:BY33544. Em:AK007467.1 Em:AK009070.1"
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/locus teg="RP23-341022.1-002"
/product="movel" transcript"
/product="movel" transcript"
                                                      This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /jocus tagg="RP23-341022.2-001"
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138391. .138510,140220. .140368,143992. .144154,
145643. .145134,146201. .146342,146440. .146579,
148619. .148793,148888. .148989,153300. .153494,
153872. .153954,154279. .154423,154509. .154613,
156487. .156536,156853. .157027,157723. .157855,
158244. .158332,158856. .158777,159775. .159898,
161443. .161650,163535. .163622,163980. .164101,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="match: ESTB: Em:BY102364.1"
                                                                                                                                                                                                                                                                                                                                                                                     Center: Wellcome Trust Sanger Institute
Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /locus_tag="RP23-341J22.1-001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /locus_tag="RP23-341J22.1-001"
|29427. .168894
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="Nos2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .178443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52534
                                                                                                                                                                                                                                                                                                                                                                 Genome Center
   Hopkins, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polyA_signal
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                                  TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                 COMMENT
             19009. 1918.19 2808. 25003.26877. 26926.27243. 224444, 24669. 24813.4849. 25003.26877. 26926.27243. 227417, 28113. 28245,28644. 28722,28986. 29167,30125. 30288, 31833. 32040,33925. 34012,34370. 34491,35526. 35674, 36440. 36544. 388170. 34491,35526. 35674, 36440. 36543,48644. 388170. 34491,35526. 35674, 36440. 36543,48664. 388170. 36490,10610. 10758, 14382. 115444,15433. 15544,16591. 16732,16830. 16969, 19382. 14544,15433. 15544,16591. 16732,16830. 16969, 19382. 14544,15433. 15544,16591. 16732,16830. 15989, 19382. 14544,15433. 15544,16591. 16732,16830. 24813,24899. 25003.26877. 26926,27243. 27417, 28113. 228245,28644. 23872,28886. 29167,30125. 33674, 36440. 36634,38684. 38782. 34012,34370. 34491,35526. 35674, 36440. 36634,38684. 38782. 34012,34370. 34491,35526. 35674, 470040=="i-NOS". 470040=="i-NOS". 470040="i-NOS". 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16673 GGCTACCAGATGCCCGATGGCACCATCAGAGGGATGCTGCCACCTTGGAGTTCACCCAG 16732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16613 CAGCGGAGTGACGGCAAACATGACTTCAGGCTCTGGAATTCACAGCTCATCCGGTACGCT 16672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALS92185
Mouse DNA sequence from clone RP23-341J22 on chromosome 11 Contains a novel gene, the Nos2 gene for inducible macrophage nitric oxide synthase 2 and the 3' end of the Lgals9 gene for soluble galactose binding lectin 9, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALS92185.35 GI:21213991
HTG; lectin; Lgals9; Nos2.
HTG; lectin; Lgals9; Nos2.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euteria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.3%; Score 98.8; DB 9; Length 38817; llarity 78.7%; Pred. No. 7.6e-13; Conservative 1; Mismatches 33; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16733 GTA-CTGACTCAGCCTCTCCTAGATCCCTGTGGGGGAGGGACCC 16775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTACCCGGCCCAGCCTCAGCCRCCGGCCATTGGGGCGGGGGGGCC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 129; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
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KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL592185
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146283 GGCTACCAGATGCCCGATGGCACCATCAGAGGGATGCTGCCACCTTGGAGTTCACCCAG 146342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /jocus_tage="RP23-12113.3-001"
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complement (17638. .17673), complement (176364. .176134),
complement (175517. .175558), complement (17438. .176134),
complement (174312. .174494), complement (17035. .172181))
/gene="Lgals9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC036147

Mus musculus chromosome 11 clone RP23-240G13 map 11, WORKING DRAFT SEQUENCE, 10 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
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                                                                                                  /jocus tage="RP23-12113.3-001"
join(AL592551.10:198512. .198683,
AL592551.10:206760. .206484, AL592551.10:210272. .210473,
AL592551.10:212034. .212144, complement (176638. .176673),
complement (176648. .176134), complement (175517. .175589),
complement (174638. .174726), complement (174332. .174434),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /locus tag="RP23-12113.3-002"
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AL592551.10:206760. 206848, AL592551.10:210272. 210473,
AL592551.10:212034. 212144, complement (178354. 178443),
complement (176538. 176673), complement (176684. 176134),
complement (17517. 175558), complement (174638. 174726),
complement (174332. 174494), complement (172035. 172181))
                                                                                                                                                                                                                                                                                                                                                                   //ocus tag="RP23-12113.3-001"
/product="lectin, galactose binding, soluble 9"
/note="match: ESTSTS: Em.AN042899.1 Em.AN04329.1
Em.AN530150.1 Em.AN541736.2 Em.BI647345.1 Em.BI657219.1 Em:BM243207.2
complement(171618)
/gene="Lgale9"
complement(174638. .174726),complement(174332. .174494),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG
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/product="lectin, galactose binding, soluble 9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 9; Length 178443;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.3%; Score 98.8; DB 9; Length 17:
78.7%; Pred. No. 6.1e-13;
ive 1; Mismatches 33; Indels
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                                    complement (171614. .172181))
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HTG; HTGS PHASE1; HTGS DRAFT.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                        /gene="Lgals9"
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Best Local Similarity 78.7
Matches 129; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product = "intric oxide synthase 2, inducible, macrophage" /protein id="Al12575.1" / protein id="Al12575.1" / db_xref="Gl:86206296" / db xref="InterPro:IPR001094" / db_xref="InterPro:IPR001433" / db_xref="InterPro:IPR001433" / db_xref="InterPro:IPR001090" / db_xref="InterPro:IPR001090" / db_xref="InterPro:IPR004030" / db_xref="InterPro:IPR004030" / db_xref="InterPro:IPR004030" / db_xref="InterPro:IPR004030" / db_xref="InterPro:IPR004030" / db_xref="InterPro:IPR0040354" / translation="WACPWFELFYKGYGSDLKEBKDINNNVKKTPCAVLSPTIQDDP KSHQNGSPQLLTGTRQPRDKFTPLEELLDPHAIBFINQYYGSFKBAKIEEHLARL TCKSKSCLGSIMNPKSLTRGPRDKFTPLEELLDPHAIBFINQYYGSFKBAKIEEHLARL
                                                                                          BAUTKEE ETGTYQLTIJDEL IF ATKAAMRNAFRCIGRIQWSNLQVPDARNCSTAQENGONIC CONTROLL OF THE CONTROLL OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLDESGSYWYKDKRLPPCSLSQALTYFLDITTPPTQLQLHKLARFATDETURQRLEAL
CQPSEYNDWKFSNNPTFLEVLEEFPSLHVPAAFLLSQLPILKPRYYSISSQDHTPSE
VHLTVAVVTYRTRDGQGPLHHGVCSTWIRNLKPQDPVPCFVRSVSGFQLPEDPSQPCI
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LKKLVATKLNLSEEQVEDYFFQLKSQKRYHEDIFGAVFSYGAKKGSALEEPKATRL"
168842. .168847
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join(AL592551.10:198515. .198683,
AL592551.10:206760. .206848, AL592551.10:210272. .210473,
AL592551.10:212034. .212144, complement (176638. .176673),
complement (176084. .176134), complement (175517. .175558),
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/fstandard_name="CTYTMOSP0000000202"
/note="match: proteins: Sw.019114 Sw.P29477 Tr:AAH62378
_r:AAL24076 Tr:097604 Tr:Q8R410 Tr:Q9BDH6 Tr:Q9N175"
       .166244,168294. .168894)
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|Jocus_tag="RP23-341J22.2-001"
                                                                            locus tag="RP23-341J22.2-001"
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10cus_tag="RP23-341J22.2-001"
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168885
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       .165284,166050.
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Quality coverage: 12.2 in Q20 bases, agarose-fp Quality coverage: 12.0 in Q20.

NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167738: contig of 26584 bp in length 67839 203042: contig of 35204 bp in length 03043 203142: gap of 100 bp 03043 203142: gap of 100 bp 13143 256456: contig of 33314 bp in length 1. 236456
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contig of 72537 bp in length
gap of 100 bn
                                                                                                                                                                                                                                                                                                                        contig of 33985 bp in length
gap of 100 bp
contig of 1045 bp in length
gap of 100 bp
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of 13750 bp in length
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of 12807 bp in length
                                                                                                                                                                                                                                                                                                                                                                                              gap of 100 bp
contig of 2936 bp in length
gap of 100 bp
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contig of 3394 bp in length
gap of 100 bp
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167739. .167838
/estimated_length=100
167839. .203042
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34086. .35130
/note="assembly_fragment"
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38167. .38266
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41761. .55510
//note="assembly_fragment"
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55611. .68417
/note="assembly_fragment"
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11661. .41760
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68518. .141054
/note="assembly_fragment"
141055. .141154
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/note="assembly_fragment
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/estimated length=100
35231. .38166
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141155. .167738
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gap of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: M13; M77815; 40% of reads Sequencing vector: Plasmid; n/4»; 60% of reads Sequencing vector: Plasmid; n/4»; 60% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 233217 bases at least Q40 Consensus quality: 24384 bases at least Q20 Consensus quality: 235022 bases at least Q20
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Web site: http://www.seq.wi.mit.edu
Web site: http://www.seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
             musculus chromosome 11, clone RP23-240G13
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Insert size: 235556; sum-of-contigs
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Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, T., Alsbrooks, S., Amin, A., Angulano, D., Anglabechi, V., Aogadi, A., Aydeli, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Baranteead, M., Benahmed, F., Baldwin, D., Bandaranaike, D., Barber, M., Barnetead, M., Benahmed, F., Baldwin, D., Bandaranaike, D., Barber, M., Barnetead, M., Benay, C., Burch, P., Burchl, Y., Calderon, E., Cadenae, V., Carter, A., Cadenae, V., Carter, A., Cadenae, V., Carter, A., Chavazo, J., Chen, G., Chen, R., Chen, R., Chen, R., Chen, T., Chen, G., Chen, R., Mantiney, R., Miner, G., Mancia, L., Loradon, P., Mantiney, R., Male, R., Marcin, R., Martin, R., Mandhiney, S., Malok, C., Manden, R., Mander, P., Martin, R., Mantine, R., Maun, P., Martin, R., Mantine, R., Maun, Morris, S., Munidasa, M., Norris, S., Park, R., Plank, R., Perez, L., Plank, R., Perez, R., Perez, L., Plank, R., Perez, R., Perez, L., Plank, R., Perez, R., Per
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Rattus norvegicus clone CH230-216J16, WORKING DRAFT SEQUENCE, 11
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                                                 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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Rattus norvegicus
     Mismatches
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Rattus norvegicus gene encoding inducible nitric oxide synthase,
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Molecular cloning and characterization of the rat inducible nitric
synchase (iNOS) gene
Gene 234 (2), 297-305 (1999)
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inducible nitric oxide synthase; iNOS gene.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Rattus norvegicus
Rattus norvegicus
Mamalia; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
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Submitted (26-JUN-1998) Keinanen R.A., A.I. Virtanen Institute,
University of Kuopio, P.O. Box 1627, FIN-70211 Kuopio, Finland
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                1 CAGCGGAGTGATGCCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                  1; Gaps
                                                                                                                                                                                                                           Query Match 38.3%; Score 98.8; DB 14; Length 236456; Best Local Similarity 78.7%; Pred. No. 5.8e-13; Aatches 129; Conservative 1; Mismatches 33; Indels 1; C
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/strain="Wistar Kyoto"
/db_xref="taxon:10116"
/clone lib="cosmid (SuperCos1) library"
<1. .15
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/usedin=AJ230462:INOS_CDS
       /note="assembly_fragment"
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/note="assembly_fragment
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/gene="iNOS"
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Keinanen, R.A.
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Matches 108; Conservative 0; Mismatches 16; Indels
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contig of 1311 b
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site:EcoRI
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Baylor Plaza, Houston, TX 77030, USA.

On Oct 9, 2002 this sequence version replaced gi:21736362.

The sequence in this assembly is a combination of BAC based reads and whole genome shedgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-casffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads Both and sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Soctt, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Siseon, I., Sitter, C.D., Smajs, D., Snead, A., Sodergren, E., Song, X.-2., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Warren, D., Waldron, L., Walker, B., Wang, J., Walght, D., Wallson, R., Wleck, Wei, X., While, F., Walght, D., Warght, R., Wei, X., Wei, X., Walght, D., Warght, R., Wu, Y., Yakub, S., Yen, J., Yoon, D., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Weinstock, G. and Gibbs, R.A. Smith, D.R., Holt, R.A., Smith, H.O., Direct, Submission
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Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Conterr project Information
Center project name: CH230-216J16
Center clone name: CH230-216J16
Center clone name: CH230-216J16
Consensus quality: 252209 bases at least Q40
Consensus quality: 252209 bases at least Q30
Consensus quality: 255370 bases; sum-of-contigs estimation
Quality coverage: 9x in Q20 bases; sum-of-contigs estimation
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NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (09-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Rat Genome Seguencing Consortium.
Direct Submission
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2 (bases 1 to 430182)
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May 13, 2003 Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 Huis sequence version replaced gi:23123790.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bom.tuc.edu/projects/rat/). Each contrig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                   Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 240200) (120 
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Consensus quality: 232006 bases at least Q40
Consensus quality: 234013 bases at least Q30
Consensus quality: 235799 bases at least Q20
Estimated insert size: 243219; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Extuse norvegicus and actives (actives) Redenta; Butheleostomi, Metatus norvegicus Actavia, Caraniate, Vertebrate; Euchecia, Eurachontoglites, Giltes; Redenta; Euchecia, Eurachontoglites, Giltes; Redenta; Caraniate, Lo 24020)

Exturgate in to 24020)

I bases in to 24020)

Muzny, D.Marie, Metzker, M.Lee, Abraacon, S., Adams, C., Alder, J., Andlen, C., Allen, H., Alberooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Balari, C., Barter, M., Barnie, Bernahed, F., Bisheno, E., Barter, M., Baraniak, D., Bandernaike, D., Barter, C., Edyler, C., Ed
        33717 GŚCTĄCCĄGATGCCCGĄTGGCĄCCATCĄGGGGATCCTGCCĄCCTTGGAGTTCACCCAG 33776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACLUSU40
Rattus norvegicus clone CH230-222O5, WORKING DRAFT SEQUENCE, 2
unordered pieces.
                                                                                                                                   61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC103040.5 GI:30580621
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                33777 GTAC 33780
                                                                                                                                                                                                                                                                                                        121 GTAC 124
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KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 39
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Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Lorensulwa, L., Loulseado, H., Lorado, R.J., Lu, X., Ma.J., Mallowa, L., Loulseado, H., Lorado, R.J., Lu, X., Ma.J., Malloy, K., Mandum, A., Mahabhari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mawhiney, S., McLeod, M.P., McNeil, T. Z., Menen, E., Milosavljevic, A., Miner, G., Menen, E., Morres, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankeris, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nankeris, S., Nankeris, S., Parks, K., Pasternak, S., Paul, H., Perez, L., Peras, C., Peres, E., Pennkoch, C., Pasternak, S., Paul, H., Perez, A., Perez, L., Pennkoch, C., Pasternak, S., Paul, M., Ren, Y., Reuter, M., Righs, F., Polndexter, A., Popovic, D., Primus, E., Pully, R., Reilly, M., Ren, Y., Reuter, M., Rose, R., Rigs, F., Riges, F., Roinfey, T., Rojas, A., Rose, M., Rose, R., Rigs, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Shvartsbeyn, R., Sutton, A., Sorelle, R., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Waish, J., Yakub, S., Yaen, J., Yoon, L., Yoon, U., Yu, F., Zhou, X., Zhou, S., Vann, D., Von, Niederhausern, A., Waiss, R., Smith, D.R., Harn, H., Shan, H., Hol, Maission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Verley, K. C.

Morley, K. C.

Direct Submission

Of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

3 (Bases I to 314746)

Direct Submission
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REFERENCE
AUTHORS
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TITLE
JOURNAL
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Sciurognathi; Muroidea; Murinae; Murinae; Rattus.

1 (Dases 1 to 314746)

Muroidea; Muroidea; Murinae; Rattus.

1 (Dases 1 to 314746)

Milen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anguiano,D., Angulano,C., Allen,C., Bandaranaike,D., Barber,M., Barnstead,M., Benamed,F., Baldmin,D., Bandaranaike,D., Barber,M., Barnstead,M., Banamed,F., Bryant,N., Bulay,C., Burch,P., Burrell,K., Calderon,E., Cardenss,V., Carter,K., Cardens,K., Carderon,E., Cardenss,V., Carter,K., Cardens,C., Cookrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dedrich,D., Denson,S., Drun,A., Durbin,K., Durbin,H., Divya,K., Egan,A., Escotto,M., Eugene,C., Evans,C.,A., Falls,T., Fan,G., Fernandez,S., Finley,W., Flaggi,N., Forbes,L., Foster,M., Gorvara,M., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Hares,C., Handilton,C., Hamilton,K., Hares,C., Milak,P., Handerson,N., Hernandez,J., Houlis,B., Howells,S., Mum,J., Johnson,B., Johnson,R., Joicken,A., Jackson,A., Jackson,L., Jackson,L., Jackson,L., Karpathy,S., Kelly,S., Khan,Z., King,L., Kovar,C., Karpathy,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86288 GGCTACCAGATGCCCGATGGCACCATCAGAGGGGATCCTGCCACCTTGGAGTTCACCCCAG 86229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314746 bp DNA linear HTG 13-MAY-2003
Rattus norvegicus clone CH230-126J7, *** SEQUENCING IN PROGRESS
***, 23 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GGCTACCAGATGCCAGATGGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.1%; Score 98.4; DB 14; Length 240200; 87.1%; Pred. No. 7.1e-13; ive 0; Mismatches 16; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACI06421.5 GI:30581088
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
                                  o.68. 10660
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   /note="wgg end_extension
clone end:T7"
6768. .. 10660
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                                                                                                                                                                                                                                                                                                                                                                                                         site: EcoRI
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Best Local Similarity
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KEYWORDS
SOURCE
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Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Daylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:24819147.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.imc.edu/projects/ratl/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table. * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

* NOTE: This sequence may represent more than one clone. Consensus quality: 286975 bases at least Q40
Consensus quality: 291712 bases at least Q30
Consensus quality: 295672 bases at least Q30
Estimated insert aize: 299042; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation Center: Baylor College of Medicine Center clone name: CH230-126J7 Assembly program: Atlas 3.0; Center project name: GKWN

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NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary only the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                             1347: contig of 13317 bp in length
1347: gap of unknown length
1965: contig of 6248 bp in length
19765: gap of unknown length
26052: contig of 6287 bp in length
26052: contig of 6287 bp in length
26152: gap of unknown length
30730: contig of 6287 bp in length
42290: contig of 1460 bp in length
42290: contig of 11460 bp in length
42290: gap of unknown length
42290: gap of unknown length
81045: gap of unknown length
81045: gap of unknown length
13540: contig of 123 bp in length
1360: gap of unknown length
1360: gap of unknown length
1360: gap of unknown length
1361: gap of unknown length
1362: gap of unknown length
1363: gap of unknown length
1393: contig of 1303 bp in length
1393: contig of 1804 bp in length
1393: contig of 1804 bp in length
1393: contig of 1804 bp in length
1493: contig of 1171 bp in length
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bp in length
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gap of unknown l
contig of 1574 b
gap of unknown l
contig of 1805 b
gap of unknown l
contig of 1121 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /estimated_length=unknown
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38779. 38210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           estimated length=unknown
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note="wgs_contig"
6053. .26152
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282339
282439
283541
283641
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286516
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288520
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; Search time 473 Seconds (without alignments) 3635.287 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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1: genesequ1980s:*
2: genesequ1990s:*
3: genesequ2000s:*
4: genesequ2001bs:*
5: genesequ2002as:*
7: genesequ2002bs:*
8: genesequ2002bs:*
9: genesequ2003bs:*
10: genesequ2003bs:*
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geneseqn2004bs:*
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Maximum DB seq length: 2000000000
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258
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111:
12:
14:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
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                                                                                                      Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	OI.	ADZ75764	AAH78096	AAH78095	ADV42931	ABX76286	ADA09713	ACF87485	ACN42845	AAC67035	AAX08434	ACA56880	AD156676	ADJ74786	ADJ74903	AAT98199	ADQ38958	AAQ66914	AAT10115	AAA34818
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	Query Match Length DB	258	1152	3462	3462	3855	3855	3855	3928	3946	4062	4062	4062	4062	4062	4070	4133	4145	4145	4145
de	Query Match	99.8	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7
	Score	257.6	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4
	Result No.	1	7	e	4	Ŋ	y	7	60	6	10	11	12	13	14	15	16	17	18	19

Claim 1; SEQ ID NO 1; 13pp; English.

Aaf20940 Human ind	Aah47966 Mouse ind	Aah47959 Human ind	Abz96634 Human ind	Abd19732 Human ind	Aaq77700 Nitric-ox	Adi32081 Human cDN	Ads84148 Human lym	Adq38959 Human SNP	Aeb69128 Human mod	Acn42844 Human dia	Acn42843 Human dia	Aaf21450 Human ind	Abz97144 Human nuc	Abd19730 Human ind	Aaa34820 Human ade	Aaf20942 Human low	Abz96636 Human nuc	Abd20500 Human pul	Aaf21436 Human enz	Abz97130 Human nuc	Abd17969 Human enz	Aac67036 Human ind	Ads88001 Tumour tr	Rat	Aaq79423 Rat induc
AAF20940	AAH47966	AAH47959	AB296634	ABD19732	AAQ77700	ADI32081	ADS84148	ADQ38959	AEB69128	ACN42844	ACN42843	AAF21450	ABZ97144	ABD19730	AAA34820	AAF20942	AB296636	ABD20500	AAF21436	ABZ97130	ABD17969	AAC67036	ADS88001	AAQ79418	AAQ79423
6	4	4	10	11	~	1	13	13	14	13	13	m	10	1	m	٣	10	11	m	10	11	4	13	0	ω,
4145	4145	4145	4145	4145	4164	4164	4164	4221	4221	4277	4278	8222	8222	8222	9513	9513	9513	9513	35384	35459	35459	4150	4150	1033	3530
46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.0	46.0	36.7	36.7
120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	118.8	118.8	94.8	94.8
20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

ADZ75764 standard; DNA; 258 BP.

ADZ75764

ADZ75764;

ds; gene; high altitude pulmonary edema; pulmonary edema; respiratory-gen.; respiratory disease; SNP detection; allelic variation; Detecting predisposition to high altitude pulmonary edema (HAPE) by amplifying intron 7 of human inducible nitric oxide synthase gene, and predicting and analyzing differences in the distribution of allelic /*tag= a /standard_name= "single nucleotide polymorphism" Human inducible nitric oxide synthase gene exon 7 SEQ ID NO:1. (COUN-) COUNCIL SCI & IND RES INDIA. Location/Qualifiers 13-NOV-2003; 2003US-00713137. 13-NOV-2003; 2003US-00713137 (first entry) Pasha AQM, Ahsan A; WPI; 2005-384299/39. US2005106573-A1 Homo sapiens. 19-MAY-2005. 28-JUL-2005 Key variation variants. exon. specification describes a method of screening for compounds that

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             high altitude pulmonary edema (HAPE). The method comprises amplifying intron 7 of the human inducible nitric oxide synthase (INOS) gene (ADZ7574) by designing and synthesizing forward and reverse oligonucleotide primers (ADZ75765+ADZ75766), and predicting and statistically analyzing differences in the distribution of the allelic variants in the populations, where GG genotype at 19480 position are at low risk of HAPE, and AA genotype at 19480 position are at HAPE. The present sequence represents exon 7 of the human iNOS gene.
  invention relates to a novel method for detecting predisposition to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening for compounds that inhibit in vitro inducible nitrogen oxide synthase useful for treating organ rejection, cerebral infarction and
                                                                                                                                                                                                                                                                                                                                                                                                                  ACAGAGTGGAGCCCAGAGGAGAACACGCAGCCCGGGCTTACAGACTCACAGGGCCCGTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence of a human inducible nitrogen oxide synthase.
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                                                                                                                                            Seguence 258 BP; 52 A; 80 C; 84 G; 41 T; 0 U; 1 Other;
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                                                                                                                                                                                  1.3e-63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     initrogen oxide synthase; iNOS; or infarction; vascular ischemia; ss.
                                                                                                                                                                     Score 257.6;
Pred. No. 1.
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100.0%; Pred
0; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      GITCCCCAGCTGTGCATC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH78096 standard; DNA; 1152 BP.
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                                                                                                                                                                                                  Conservative
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hes 258;
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         inhibit in vitro inducible nitrogen oxide synthase (iNOS) activity. The method comprises contacting the iNOS monomer with a candidate compound, and selecting those compounds that bind to it. As dimerisation of INOS is the final step of the acquisition of the iNOS enzymatic activity, iNOS inhibitor compounds can can be quickly and efficiently screened. The inhibitors are useful for treatment and prevention of organ rejection, cerebral infarction and vascular ischemia. The present sequence encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The specification describes a method of screening for compounds that inhibit in vitro inducible nitrogen oxide synthase (INOS) activity. The method comprises contacting the INOS monomer with a candidate compound, and selecting those compounds that bind to it. As dimerisation of INOS is
                                                                                                                                                                                                                                                                     438
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                                                                                                                                                                                                                                                                                                                    439 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 498
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                                                                                                                                                                                                                                                                      379 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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                                                                                                                                                                             Length 1152;
                                                                                                                                                  Sequence 1152 BP; 275 A; 326 C; 322 G; 229 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inducible nitrogen oxide synthase; iNOS; organ rejection; cerebral infarction; vascular ischemia; 88.
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                                                                                                                                                                           Score 120.4; DB 4;
Pred. No. 2.6e-24;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of a human polypeptide.
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1. .3462
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                                                                                                                                                                                                            Conservative
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                                                                                                                                                                             Query Match
Best Local Similarity
Matches 121; Conserv
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Length 3462;

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Query Match
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ABX76286
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                                                                                                                                                                                                                                                         61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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                                                                                                                                                                                                                            804
                                                                                                                                                                                                                                                                                        864
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inhibitor compounds can can be quickly and efficiently screened. The inhibitors are useful for treatment and prevention of organ rejection, cerebral infarction and vascular ischemia. The present sequence was used in the course of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New microarray comprising probes for genes involved in psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a condition associated with PNI activity, e.g., inflammatory or infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     microarray; psychoneuroendocrinimmune; chronic fatigue;
non-insulin dependent diabetes; allergy; immune disorder; inflammation;
cancer; neoplasm; infection; expressed sequence tag; ss.
                                                                                                                                                                                                                                                                             GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG
                                                                                                                                                                                                                    CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCGCTATGCT
                                                                                                                                                                                               1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                   Gaps
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                                                                                                                                     Length 3462;
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                                                                                                       Sequence 3462 BP; 801 A; 1027 C; 962 G; 672 T; 0 U; 0 Other;
                                                                                                                                                                 Indels
                                                                                                                                   DB 4;
                                                                                                                                   46.7%; Score 120.4; DB 4 99.2%; Pred. No. 3.3e-24;
                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human psychoneuroendocrinimmune
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                                                                                                                                                     Best Local Similarity 99.2
Matches 121; Conservative
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                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                        866
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                                                                                                                                      Query Match
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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polyuncleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples, Lung cancer-associated polymeted polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema; antinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
                                                                                                         804
                                                                                                                                             GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTAG 120
                                                                                                                                                                                 864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
                                                                                                                                                                    CAGCGGAGTGATGGCAAGCACGACTTCCCGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                       Gaps
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                                       Indels
Score 120.4; DB 14
Pred. No. 3.3e-24;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 22; Page 301-302; 453pp; English.
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10-MAY-2001; 2001US-0290492P.
09-NOV-2001; 2001US-033245P.
13-NOV-2001; 2001US-035666P.
29-NOV-2001; 2001US-0334370P.
46.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                     Matches 121; Conservative
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Sequence 3855 BP; 894 A; 1136 C; 1067 G; 0 T; 758 U; 0 Other;

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lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polymucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated polymucleotides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to screening assays for testing nutraceuticals. The invention provides methods for detecting RNA in cells exposed to various types, concentrations, and combinations of nutraceuticals using the INVADER detection assay. The INVADER detection assay detects and quantifies test gene mRNA. The INVADER assay detection reagents comprise a probe and an INVADER oligonucleotide. The invention provides a high throughput, sensitive, quantitative, and cost-effective method of testing nutraceuticals. The present sequence represents human nitric oxide synthase 2A (NOS2A) mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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INVADER detection assay; human; nitric oxide synthase 2A; NOS2A; ss.
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                                                                                                                                                                                                                                                                                                                    Sequence 3855 BP; 894 A; 1136 C; 1067 G; 758 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human nitric oxide synthase 2a (NOS2A) mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                      46.7%;
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                                                                                                                                                                                                                                                         invention
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ADA00930

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The invention relates to a novel method for in vitro detection of systemic inflammatory response syndrome (SIRS). The method comprises detecting abnormal expression of disease-related genes, or their associated peptides. The method of the invention demonstrates antibacterial, immunosuppressive and antiinflammatory applications and may be used for early differential disaposis, monitoring progression, assessing risk, assessing the likely response to treatment and for post mortem disaposis of systemic inflammatory response syndrome, sepsis and sepsis like conditions. The recombinant or synthetic acid sequences of the invention, or derived proteins or peptides, may be useful as calibrants in assays for the specified diseases, for evaluating activity or toxicity in screening for active agents and/or for preparation of agents for treatment or prevention of the specified diseases. The current sequence is that of a human SIRS/sepsis disapostic marker DNA fragment of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published
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                                                                                                                                                             In vitro detection of systemic inflammatory response syndrome and related conditions, for e.g. monitoring progression, comprises detecting abnormal expression of disease-related genes.
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                                      Gaps
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   Length 3855;
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                                   Indels
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 DB 9;
 46.7%; Score 120.4; DB 9
80.3%; Pred. No. 3.4e-24;
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                                    23; Mismatches
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08-AUG-2003; 2003DE-01036511.
02-SEP-2003; 2003DE-01040395.
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                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                    98; Conservative
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Query Match
Best Local Similarity
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diagnose a particular condition, disease or disorder associated
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                                                                                                                                                                                               GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gietzen D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
   pot sequences. Furthermore, a number of arbitrary SEQ ID NO.8 are disclosed within the specification, however, these have not been taken into account during indexing due to inconsistencies in application and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kirton ES;
                                                                                                                                                                             1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                               Gaps
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                                                                                                                DB 13; Length 3855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human diagnostic and therapeutic polynucleotide SEQ ID NO:1720.
                                                                                  Sequence 3855 BP; 897 A; 1134 C; 1065 G; 759 T; 0 U; 0 Other;
                                                                                                                                               Indels
                                                                                                             Score 120.4; DB 13;
Pred. No. 3.4e-24;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                        ACN42845 standard; cDNA; 3928
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                                                                                                                Query Match
Best Local Similarity 99.2%;
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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ACN42845
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used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorder, autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence data for this patent is not represented the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a novel method of treating influenza virus infection by administering an antisense oligonucleotide directed at the human inducible nitric oxide synthase (INOS) mRNA. This is useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; influenza virus; antisense; inducible nitric oxide synthase; iNOS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating viral influenza with antisense oligonucleotides that hybridize with inducible nitride oxide synthase mRNA and inhibit synthesis of the enzyme, reducing the production of nitric oxide in lungs.
                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGCGGAGTGATGGCAAGGACGACTTCCGGGTGTGGAATGCTCAGCTCATCCTTTGCT
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                                                                                                                                                                                                                                        directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
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                                                                                                                                                                                                                                                                          Sequence 3928 BP; 928 A; 1151 C; 1086 G; 763 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                     Score 120.4; DB 13; Length
Pred. No. 3.4e-24;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human inducible nitric oxide synthase coding sequence #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preventing the symptoms of influenza infection
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                                                                                                                                                                                                                                                                                                                            46.7%;
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                                                                                                                                                                                                                                                                                                                                                Local Similarity
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Length 4062;

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The invention relates to a combination which, comprises a number of polynucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an array element in a microarray for monitoring the expression of a number of target polynucleotides. The microarray is particularly useful in the diagnosis and treatment of cancer and immunopathology and neuropathology. The microarray is useful in diagnostics and treatment regimens, drug discovery and development, toxicological and carcinogenicity studies, forensics and pharmacogenomics. The microarray is also useful for
                                                                                                                                                                                                                                                                                                                                                                             850 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGAAATGCTCAGCTCATCCGCTATGCT 909
antioxidising agent. The methods can be used for protecting cells against immunotoxicity mediated by, e. g. 1L-1 beta, 1L-1 alpha, gamma IFN, TNF alpha, TNF beta, 1L-8, 1L-7, 1L-9, 1L-14, 1L-17, granulocyte-macrophage colony stimulating factor or monocyte chemoattractant protein-1. The methods can be used for the treatment of e.g. insulin-dependent diabetes mellitus (IDDM), NIDDM, obesity, wasting syndromes, short stature, osteoporosis, inflammatory diseases, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   910 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     signalling pathway population; cancer; adenocarcinoma; leukaemia; immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
                                                                                                                                                                                                                                                                                                                                                   1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Combination of polynucleotide probes, useful as array elements in microarray for monitoring the expression of a number of target
                                                                                                                                                                                                             Sequence 4062 BP; 966 A; 1178 C; 1099 G; 819 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human signalling pathway polynucleotide probe SEQ ID NO 1478.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probe; ss; array element; Parkinson's disease;
                                                                                                                                                                                                                                                      46.7%; Score 120.4; DB 2; 99.2%; Pred. No. 3.4e-24; ive 0; Mismatches 1;
                                                                                                                                                                  diseases, or neurodegenerative diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACA56880 standard; cDNA; 4062 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-00016434
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                                                                                                                                                                                                                                                                                                     Conservative
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Best Local Similarity
Matches 121, Conserv
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                                                                                                                                                                                                             GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                     GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 864
                                                                                                                                                                745 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Manganese containing superoxide dismutase; MnSOD; IDDM; diabetres mellitus; treatment; therapy; nitric oxide; NO; beta cell; fatty acids; lipotoxic; cytocoxic; cytokine; osteoporosis; inflammatory disease; autoimmune disease; neurodegenerative disease; ss.
                                                                                                                     CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protection of mammalian cells against immunotoxicity or lipotoxicity used for treating, e.g. diabetes, obesity, wasting syndromes, osteoporosis, inflammatory diseases, autoimmune diseases or
                                                                            Gaps
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                            Length 3946;
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, Lee Y;
                                                                          1; Indels
                          Score 120.4; DB 4;
Pred. No. 3.4e-24;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clark SA, Ne
, Ohneda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inducible nitric oxide synthase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX08434 standard; DNA; 4062 BP.
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98US-0076676P,
                          46.7%;
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Shimabukuro M, Koyama K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
           Query Match
Best Local Similarity 99.2'
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03-MAR-1998;
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monitoring progression of diseases and for developing sophisticated profiles for the effects of currently available therapeutic drugs. The combination is also useful for purifying a subpopulation of mRNAs, cDNAs and genomic fragments and in research and diagnostic applications. The array can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose various diseases including cancer e.g. adenocarcinoma and leukaemia, immunopathies e.g. AlDS and asthma, neuropathies e.g. Alzheimer's disease and Parkinson's disease. The present sequence represents a polynucleotide probe of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; probe; ss; receptor-like polypeptide; transducing polypeptide; effector-like polypeptide; cancer; immunopathology; neuropathology; drug development; toxicology; carcinogenicity; signalling pathway polypeptide; adrenal gland; bladder; bone; bone marrow; brain; breast; cervix; tumour; immunopathology; diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology; dementia; amnesia; epilepsy; Alzheimer's disease; depression.
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                                                                                                                                                                                                                          Beqdata.uspto.gov/sequence.html?DocID=06500938B1
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                                                                                                                                                                                                                                                                                                                     Local Similarity 99.2
Les 121; Conservative
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Matches
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Claim 6; SEQ ID NO 1478; 73pp; English

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The invention relates to a composition of polynucleotide probes comprising first polynucleotide probes comprising at least a portion of a gene encoding a receptor-like polypeptide, second polynucleotide probes comprising at least a portion of a gene encoding a transducing comprising at least a portion of a gene encoding a refector-like polypeptide. The probes of the composition are useful as array elements in a microarray for monitoring the expression of target polynucleotides. The microarray for monitoring the expression of target polynucleotides. The microarray is useful in the diagnosis and treatment of cancer, an immunopathology or a composition are associated for monitoring the progression of diseases to micropathology. It can also be used for drug discovery and development, consuropathology. It can also be used for monitoring the progression of diseases that may be associated with the altered expression of signalling pathway polypeptides. The composition can also be used to purify a subpopulation of minkas, cDNMs, or genomic fragments in a sample. The expression profile communopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or ulcarative colities, or a neuropathology, e.g. dementia, amnesia, culcarative colities, or a neuropathology, e.g. dementia, amnesia, content of the progression. This sequence represents a human polynucleotide probe of the invention. Note: The sequence data for chis patent did not form part of the printed specification but was
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respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
gene therapy; marker gene; gene; ds.
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Best Local Similarity 99.2%; Pred. No. 3.4e-24;
Matches 121; Conservative 0; Mismarchar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4062 BP; 966 A; 1178 C; 1099 G; 819 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   segdata.uspto.gov/sequence.html.
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20-MAR-2003; 2003JP-00077212.
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ADJ74786
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Ното варіенв

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The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy comparing the expression level of the marker gene in a biological sample from a healthy constructive pulmonary disease. The marker gene comprises: (a) a group of genes (51) whose expression levels increase when respiratory epithelial colls are stimulated with interleukin-13. Also described: (l) a group of genes (52) whose expression levels decrease when respiratory epithelial colls are stimulated with interleukin-13. Also described: (l) a reagent (l) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for soreening for andidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (3) an inducer that induces bronchial asthma in a mouse; (5) a constructive pulmonary disease; (4) an inducer that induces bronchial asthma or chronic obstructive pulmonary disease; (c) asthma or chronic obstructive pulmonary disease, comprising the compound, a marker gene or an antisense nucleic acid corresponding to a portion of the marker gene or an antisense nucleic acid corresponding to a portion of the marker gene or an antisense nucleic acid corresponding to a portion of the marker gene a ribozyme, a polynucleotide that suppresses the expression of the gene through an RNAi effect or an antibady recognising a probe has been immobilised to assay a marker gene. (1) has respiratory content encoded by a marker gene; and (7) a DNA chip for testing for corresponding to a portion of bronchial asthma or chronic obstructive pulmonary disease. The present is useful for testing for or screening to a procession of the seventing to a procession of the sequence is used in the exemplification of the present invence is use
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respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
gene therapy; marker gene; gene; ds.
                                                                     disease by
                                                                                         comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                     for bronchial asthma or chronic obstructive pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4062 BP; 966 A; 1178 C; 1099 G; 819 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 3.4e-24;
0; Mismatches 1
                                                                                                                                                                                             Claim 1; SEQ ID NO 38; 241pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ74903 standard; DNA; 4062 BP
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Matches 121; Conservative
                       WPI; 2004-193155/19
                                                                                                                                                  healthy subject.
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                                                                       Testing
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The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises or chronic obstructive pulmonary disease. The method comprises cor chronic obstructive pulmonary disease. The marker gene in a biological sample from a subject, comparing the expression level of the marker gene in a biological sample from a healthy comparing the expression levels from a biological sample from a healthy compared to the marker gene in a biological sample from a healthy compared to the marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial colls are stimulated with interleukin-13. Or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13. Also described: (1) a reagent (1) for certing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to trreat bronchial asthma or chronic obstructive pulmonary disease; (5) a manimal model for bronchial asthma or chronic obstructive pulmonary disease; (5) a conting an animal model for bronchial asthma or chronic obstructive pulmonary disease, compound, a marker gene or an antisense nucleic acid corresponding to a portion of the marker gene or an antisense nucleic acid corresponding to a portion of expression of the gene through an RNAi effect or an antibod by a marker gene; and (1) a DNA chip for testing for expression of the gene through an RNAi effect or an antibod or a chronic obstructive pulmonary disease, on which a proche in encoded by a marker gene; and (1) a DNA chip for testing for a protein encoded by a marker gene; and (1) a DNA chip for testing for a protein encoded by a marker gene; and (1) a DNA chip for testing for a protein encoded by a marker gene; and (1) a DNA chip for testing for a protein encoded by a marker gene; and (1) a DNA chip for testing for a protein encoded by a marker gene; and (1) a DNA chip 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and antiasthmatic activities, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present sequence is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Testing for bronchial asthma or chronic obstructive pulmonary disease by comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a
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                                                                                                                                                                                                                                                                                                                                     Nagai H, Izuhara K;
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                                                                                                                                                                                                                                                                                                                                     Kubo H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 155; 241pp; English.
                                                                                                                                                                                                                                                                                                                                     Yamaya M,
                                                                                                                                                                                                      06-AUG-2002; 2002JP-00229312.
20-MAR-2003; 2003JP-00077212.
                                                                                                                                                      04-AUG-2003; 2003EP-00254857
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Matches 121; Conservative
                                                                                                                                                                                                                                                                                    (GENO-) GENOX RES INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      healthy subject.
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ADQ38958 standard; DNA; 4133 BP.

RESULT 16 ADQ38958 (first entry)

18-NOV-2004

ADQ38958;

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This cDNA sequence includes a coding region for human penis inducible nitric oxide synthetase (HPiNOS) (see AAW36113). It was isolated by reverse transcription of mRNA from human penile smooth muscle cells with iNOS antisense primers, combined with PCR amplification of the resulting cDNA fragments. The invention is directed to a method of treating crectile dysfunction in a patient by providing an agent capable of treating erectile dysfunction, and introducing an effective amount of the agent into the penile tissue of the patient. Preferably, the agent induces cavernosal smooth muscle relaxation, and/or produces an increase in the level of NOS in tissue. Preferably, the NOS is iNOS, and the agent is introduced into the corpora cavernosa of the penis. The agent is introduced into the corpora cavernosa of the penis. The agent is preferably an NOS inducer, an NOS protein such as HPINOS, a cDNA encoding an NOS such as HPINOS, or cDNA-transformed penile cells, especially corpora
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treatment of erectile dysfunction - by introducing an agent into penile tissue, particularly for inducing cavernosal smooth muscle relaxation or increasing NOS levels.
                                                                                                                            Nitric oxide synthetase; NOS; iNOS; HPiNOS; human; erectile dysfunction; impotence; gene therapy; corpora cavernosa; relaxant; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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Pred. No. 3.4e-24;
0; Mismatches 1
                                                                                                Human inducible nitric oxide synthetase cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 14; Page 35-38; 53pp; English.
                                                                                                                                                                                                           Location/Qualifiers
197. .3658
/*tag= a
AAT98199 standard; cDNA; 4070 BP
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                                                                                                                                                                                                                                                                                                                                                                                    96US-0017373P.
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                                                                 11-MAY-1998 (first entry)
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nes 121; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-008577/01
                                                                                                                                                                                                                                                                                                                                                                                                                                      RAJF/) RAJFER J.
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                                                                                                                                                                                                                                                                                                                                                   09-MAY-1997;
                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                   WO9742965-A1
                                                                                                                                                                                                                                                                                                                                                                                    10-MAY-1996;
                                                                                                                                                                                                                                                                                                                    20-NOV-1997.
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                                  AAT98199;
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Matches
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The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention altered risk for myocardial infarction in the individual. The invention correlated represence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention of the specification or its comprising an uncleotides where one of the nucleotides is an SNP given in the specification and in the specification, an isolated polypeptide or comprising an amino acid sequence given in the specification, an antibody that specification and which is between about 16 and 1000 nucleotides in the copyuncleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule, a method of detecting an variant polypeptide; and comprising the copyuncleotide, and indecided and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting an variant polypeptide; and an enzyme; a method of detecting an SNP in an uncleic acid molecule; a method of detecting an variant polypeptide; and an enzyme; a method of detecting an SNP in an uncleic acid soft the invention may be used in gene therapy. The mycardial infarction. The novel detection method has an increased or method is useful in identifying an individual who has an increased or method is useful in identifying an individual who has an increased or composition for treating or preventing mycardial infarction. This composition for treating or preventing mycardial infarction. This esquence was not shown in the specification. The sequence has come from a electronic sequence listing downloaded from the MIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.
                                                                                                         Human SNP containing myocardial infarction-associated gene, SEQ ID 621.
                                                                                                                                                     Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; SEQ ID NO 621; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Iakoubova 0;
                                                                                                                                                                                                                                                                                                                                                                          22-DEC-2003; 2003WO-US040978.
                                                                                                                                                                                                                                                                                                                                                                                                                      20-DEC-2002; 2002US-0434778P.
10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Devlin JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (APPL-) APPLERA CORP
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                                                                                                                                                                                                                                                                                 WO2004058052-A2.
                                                                                                                                                                                                                                     Homo sapiens.
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Length 4133;

Score 120.4; DB 13; Pred. No. 3.4e-24;

46.7%;

Query Match Best Local Similarity

RESULT 17

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1011 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 1070
    951 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A cDNA clone (AAT10115), designated pHINOS, codes for the human hepatocyte inducible nitric oxide synthase (INOS = AAR88464). It was obtd. by isolating mRNA from hepatocytes induced in vitro for INOS biosynthesis, preparing a cDNA library in a phage lambda Zap II vector, and screening with a cross-species iNOS probe. The cDNA can be used to prepare iNOS for therappeutic use. Alternatively, it is used in gene therapy strategies for treatment of vascular occlusive disease associate with atherosclerosis, vascular bypass and diabetes mellitus, tumor cell growth, and microbial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inducible nitric oxide synthase gene - useful in gene therapy to treat, e.g. vascular occlusive disease and cancer.
                                          GGCTACCAGATGCCAGATGCCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                              Inducible nitric oxide synthase; iNOS; hepatocyte; gene therapy; vascular occlusive disease; cancer; infection; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 120.4; DB 2;
Pred. No. 3.4e-24;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                          Nitric oxide synthase cDNA clone pHINOS.
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207. .3668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 72; Page 53-58; 91pp; English.
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Matches 121; Conservative
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                                                                                                                                               999 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 1058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ66914 is from human hepatocyte inducible nitric oxide synthase cDNA clone pHINOS from lambda Zap II CDNA library. The original source was induced human hepatocyte RNA. HINOS cDNA plasmid is pref. transformed in E. coli SOLN (APTC 69126). The inventors claim a clone with the cDNA sequence in AAQ66914 and a cDNA clone which encodes AAR55764. The cloning and expression of a human tissue nitric oxide synthase cDNA provides a source of the enzyme for therapeutic purposes, for example to prevent the hypotensive shock seen with sepsis. (Updated on 25-WAR-2003 to correct PN
                                                                                                                      GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                939 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence of the cDNA clone for human hepatocyte inducible nitric oxide
                                        1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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    Gaps
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  1; Indels
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0; Mismatches
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207. .3668
/*tag= a
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(first entry)
  Matches 121; Conservative
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28-DEC-1994
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Matches 121;
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The present invention describes a new composition comprising an antisense oligonucleotide (DN) with low adenosine (up to 15%), which targets and/or nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, and/or antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, cantiasthmatic, cytostatic allergies associated with inflammation, constituted airway, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating c.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive cylmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including CC breast and prostate cancer. The reduction of the adenosine content of the CONS reduces side effects. The A-containing ONS break down with the conceptore side effects. The A-containing ONS break down with the conclosusing which correspond to SEQ ID NO:1 to 2815, and then the last 185 conclosusly mamed sequences listing from the previously mamed sequences. SEQ ID NO:1 to 1880 (AAA3532 or AAA3392) are specifically claimed ONS from the previously mamed sequences. SEQ ID NO:1 to 1880 (AAA3232) concert of the match content in the interest invention do not match iterior which their corresponding SEQ ID NO: sequences given in the sequence jiering the present invention of the match content of the present invention of the present invention of the present invention of the present interest sequences given in the disclosure of the present invention of the present invention of the present invention of the present interest sequences given in the disclosure of the presen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                            Human; adenosine receptor; low adenosine antisense oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                    phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                                                                      Human adenosine receptor related polynucleotide SEQ ID NO:2507.
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                                                                                                                                                                                AAA34818 standard; DNA; 4145 BP
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121 GT 122
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                                                                                                                                                                                                                                                                                                                                                                  GGCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; airway disorder; bronchoconstriction; lung inflammation; human; airway disorder; bronchoconstriction; lung inflammation; bronchoconstriction; lung inflammatory; immunosuppressive; antiathmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base.
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                                                                                                                                                                                                                           CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human inducible nitric oxide synthase polynucleotide fragment #2507.
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                                                                                            Length 4145;
                     Sequence 4145 BP; 968 A; 1203 C; 1126 G; 848 T; 0 U; 0 Other;
                                                                                                                                                           Indels
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                                                                                 Score 120.4; DB 3,
Pred. No. 3.4e-24;
0; Mismatches 1,
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                                                                                            46.7%;
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                                                                                            Query Match
Best Local Similarity
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chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, binding proteins, adenosine receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensine, growth factors, vascoative peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction surfactant hypoproduction) and/or lung inflammation, allergy(ies) and/or condition selected from pulmonary vasocoated with a disease or condition selected from pulmonary vasocoatriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CP), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (CPPD),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1011 GCCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 1070
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                                                                                                                                                                                                                                                                                                                                 and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                               pulmonary transplantation rejection, pulmonary infections, bronchitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antisense oligonucleotide; inducible nitric oxide synthase; modulate expression; immunomodulator; antidiabetic; cardiovascular; cardiant; neuroprotective; vasotropic; ischaemia; reperfusion injury; 2'-0-methoxyethyl; phosphorothioate; mouse; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                46.7%; Score 120.4; DB 3; Length 4145; 99.2%; Pred. No. 3.4e-24; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4145 BP; 968 A; 1203 C; 1126 G; 848 T; 0 U; 0 Other;
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207. .3668
//ttag // product = "inducible nitric oxide synthase"
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                                                                                                                                                                                                                                                                                                                                                                            the present invention
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1011 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 1070
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                                                                      New antisense oligonucleotides for modulating the expression of inducible nitric oxide synthase in cells or tissues, particularly useful for treating e.g. immunological, cardiovascular or neurological disorders, or
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/product= "inducible nitric oxide synthase"
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46.7%; Score 120.4; DB 4;
Best Local Similarity 99.2%; Pred. No. 3.4e-24;
Matches 121; Conservative 0; Mismatches 1;
                                                                                                                                                                         Example 13; Page 98-103; 144pp; English
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                    WPI; 2001-465340/50
                                    P-PSDB; AAG64498
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23-APR-2002; 2002WO-US013135.
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Best Local Similarity 99.2
Matches 121, Conservative
                                                                                                                      WPI; 2003-229219/22.
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                                                                                                                                                                                    ubiquinone
                                                                                          Miller S,
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                                                                                                                   New antisense oligonucleotides for modulating the expression of inducible nitric oxide synthase in cells or tissues, particularly useful for treating e.g. immunological, cardiovascular or neurological disorders, or
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                                                                                                                                                                                                                                                                                                                                                                             useful for research and diagnostics. The present sequence is that of human inducible nitric oxide synthase (GenBank accession number L09210)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGTATGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4145 BP; 968 A; 1203 C; 1126 G; 848 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human inducible nitric oxide synthase nucleic acid.
                                                                                                                                                                                       Example 13; Page 92-97; 144pp; English.
                                                      Cowsert LM
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  24-JAN-2000; 2000US-00490208
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                             (ISIS-) ISIS PHARM INC
                                                      Dean NM,
                                                                                WPI; 2001-465340/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                              P-PSDB; AAG64497
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                                                      Bennett CF,
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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiliflammatory steroid and ubiquinone. A composition of the invention has antilinflammatory and ubiquinone. A composition may have a immunosuppressive, and cytostatic activity. The composition may have a cuse in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antilifammatory steroid in a subject. for reducing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of upiquinone or lung surfactant in a subject's tissue, or treating bronchoonstriction. In a subject of the pronchodilation, increasing levels of adenosine lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1010
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                                                                                                                                                                                                                                                                                                                                                                                                               Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        951 cagcedagrearedcaaecaccacriccedereredaarecrcaecrcarccecrarecr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 11876; 872pp; English.
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                                                                                                                                                                               Katz E,
                                                                                                                                                                               Li Y, Sandrasagra A, Ka
Tang L, Shahabuddin S;
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24-APR-2001; 2001US-0286137P.
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                                                                                            (EPIG-) EPIGENESIS PHARM INC
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This invention describes a novel composition (a) a first active agent, comprising oligonucleotides, effective for alleviating comprising oligonucleotides, effective for alleviating bronchoconstruction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The oligonucleotides are derived from a gene encoding or regulating expression of a target polypeptide associated with lung airway or lung airwaton or cancer and can be anti-sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery device, in separate containers, (b) the oligonucleotides, (c) instructions for adding a carrier and for use of the kit. The composition of the invention has antiallergic, antiinflammatory, antiachmatic, analgesic, hypotensive, immunosuppressive and cytostatic activity, is a beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered composition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to reduce the amount of target polypeptide present in the lungs. The pulmonary obstruction, and/or bronchoconstriction and/or lung inflammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vascconstriction, confirming and as pulmonary vascconstriction, confirming and administration, pulmonary incections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to thymidines present in the target RNA serves to prevent the breakdown of the oligonucleotides into products that free adenosine into the system e.g., lung, brain, heart, kidney, ecc, tissue environment and thereby, to prevent any unwanted effects due to it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1011 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 1070
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respiratory distress syndrome, allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pharmaceutical composition for treating asthma, has antisense oligonuclectide containing less percentage of adenosine, targeted trucleic acids associated with lung airway or lung dysfunction, and
                                                                                                                                                                                                                                                                                                                                                                                E, Pabalan J, Aguilar D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11; Length 4145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 15; SEQ ID NO 11876; 763pp; English.
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Tang L, Shahabuddin S;
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                                                                                                                                                                                                                                                                                   24-APR-2001; 2001US-0286036P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bronchodilating agent
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Theal Similarity
                                                                                                                                             WO200285309-A2
                                                                                                 Homo sapiens.
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nitric-oxide-synthase. cDNA was generated and used to construct a library in lambda ZAPII. This was screened with a 650 bp fragment of mouse inducible NO-synthase cDNA to identify the full-length clone pBSHSINOS. The insert was transferred to pSVL to give a vector capable of expressing NO-synthase in CHO cells under control of a hererologous constitutive promoter. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                    Nitric-oxide-synthase; NO-synthase; NOS; chondrocyte; interleukin-1-beta; pBSHSINOS; arthritis; hypertension; septic shock; inflammation; ischemia; dementia; obesity; tumor; agonist; antagonist; vector; CHO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human inducible nitric oxide synthase - useful for identifying enzyme inhibitors and stimulators, and for diagnosis and treatment of e.g. viral
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Chinese hamster ovary, cell culture, ds
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                                                                                                                                                                                           Nitric-oxide-synthase pBSHSINOS clone.
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226. .3687
/*tag= a
                                                                                            AAQ77700 standard; cDNA; 4164 BP.
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                                                                                                                                                                 (first entry)
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Best Local Similarity 99.2
Matches 121; Conservative
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                                                                                                                                                    (revised)
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121 GT 122
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09-MAY-1995
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Gaps

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Mismatches

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Matches 121; Conservative

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The invention relates to a composition comprising a plurality of CDNAs for detecting the altered expression of genes in an immunological invention also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, contacting the treatment of an immunopathological condition in a sample, contacting the treatment of an immunopathological conditions to form one or more hybridisation complexes, detecting the nucleic conditions to form one or more hybridisation complexes and comparing the levels of the detected in a non-diseased sample, where an altered level of the detected hybridisation complexes correlates with the presence of an immunopathological condition. Also disclosed are an expression profile comprising a microarray and a plurality of detectable complexes and the comprision of target polymucleotides. The microarray for monitoring are useful as hybridisable array elements in a microarray for monitoring the diagnosis of an immunopathology, such as Crohn's disease, asthma, culerative colitis, hypereosinophila, irritable bowel syndrome, culerative colitis, hypereosinophila, irritable bowel syndrome, carcinogenicity studies, forensics or pharmacogenomics. The microarray may also be used in drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. The composition may also be used in purification of a subpopulation of a fundation. Mote: The sequence cata for this patent did not form part of the printed specification but was obtained in electronic format directly the printed parent of the printed format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A composition comprising a plurality of cDNAs, useful for detecting altered expression of genes in an immunological response or for diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma or osteoarthritis.
                                                                                                                                                                                                       Human, gene, ss; immunological response; immunopathological condition; Crohn's disease; asthma; ulcerative colitis, hypereosinophilia; irriteable bowel syndrome; osteoarthritis; rheumatoid arthritis; acute monocytic leukaemia; antiinflammatory; antiathmatic; antiulcer; osteopathic; antiarthritic; antirheumatic; cytostatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 1407; 50pp; English.
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                                          ADI32081 standard; cDNA; 4164 BP
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                                                                                                                            (first entry)
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                                                                                                                                                                      Human cDNA #1407.
                                                                                                                                                                                                                                                                                                                                                                                    US6607879-B1.
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                                                                                    ADI32081;
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RESULT 26
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1030 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG 1089
                                 970 cascosastratoscaascacacerrecesereresaarecreascrearecrates 1029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New compositions having a number of first, second and third polynucleotide probes, useful in research and diagnostic applications in cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis and
                                                                            GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG
1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         se; gene; human; immunological response; blood cell; cancer; immunopathological; AIDS; allergy; anaemia; asthma; atherosclerosis; bronchitis; ulcerative colitis; diabetes; multiple sclerosis; osteoporosis; pancreatitis; infection; arthritis; lymph node.
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                                                                                                                                                                                                                                                                                                  ADS84148 standard; cDNA; 4164 BP.
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Score 120.4; DB 11; Length 4164; Pred. No. 3.4e-24;

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Homo sapiens.
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Bjerke LM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual the invention caltered risk for myocardial infarction in the individual. The invention caltered risk for myocardial infarction in the individual. The invention caltered risk for myocardial infarction in the individual. The invention caltered risk for myocardial infarction in the individual. The invention caltered risk in the specification or its complement and encoding any one of the amino the specification or its complement and encoding any one of the amino calt sequences given in the specification; an antibody that specification and which is between about 16 and 1000 nucleotides in length, a kit for detecting an SNP in a nucleic acid molecule, a method of detecting an SNP in a nucleic acid molecule, a method of detecting an variant polypeptide; and molecule, a method of detecting an variant polypeptide; and method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection may be used in gene therapy. The method is useful in identifying an individual who has an increased or
                        970 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1029
                                                                                                 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                               Human SNP containing myocardial infarction-associated gene, SEQ ID 622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myocardial infarction, detection, single nucleotide polymorphism, SNP, cardiant; gene therapy, human; gene; ds.
CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; SEQ ID NO 622; 145pp; English.
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                                                                                                                                                                                                                                                                                             ADQ38959 standard; DNA; 4221 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-DEC-2002; 2002US-0434778P.
10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.
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                                                                                                                                                        GT 122
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1068
decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This polynucleotide sequence represents a human myocardial infarction associated gene containing one or more SNP's of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modulating agents useful for diagnosing or treating, for e.g. cancer, comprises screening for agents that modulate the activity of a modifier
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Screening; insulin growth factor receptor; IGFR; diagnosis; cancer;
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                                                                                                                                                                                                                                                                                                                46.7%; Score 120.4; DB 13; Length 4221; 99.2%; Pred. No. 3.4e-24; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                Sequence 4221 BP; 998 A; 1216 C; 1133 G; 857 T; 0 U; 17 Other;
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Jin Y,
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J, Hitz BC, Lickteig K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human modulator of IGFR pathway polynucleotide #5.
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12-MAR-2004; 2004US-0552634P.
21-JUN-2004; 2004US-0581696P.
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                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 99.2%;
Matches 121; Conservative
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Adamkewicz
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WO2004023973-A2
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Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Elegace RT, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LLI,
Lagace RE, Spiro PA, Stewart EA, Mingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
Patury S, Shi X, Suarez CJ;
agent, the system provides a reference activity and detecting a test agent-biased activity of the assay system, where a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate IGFR pathway modulating agent. The invention also relates to methods for modulating an IGFR pathway of a cell or in a mammallain cell and a method for diagnosing a disease in a patient. The methods are useful for diagnosing or treating cancer or for identifying modulators of an IGFR pathway, which may be utilized as therapeutic targets for disorders associated with defective IGFR function, such as polynucleotide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                        Query Match
46.7%; Score 120.4; DB 14; Length 4221;
Best Local Similarity 99.2%; Pred. No. 3.4e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human diagnostic and therapeutic polynucleotide SEQ ID NO:1719.
                                                                                                                                                                                                                                                                                                Sequence 4221 BP; 1001 A; 1221 C; 1138 G; 861 T; 0 U; 0 Other;
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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therappy. The human clasmostic and therapeutic polynucleotides (dithp) or polyneptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, questioning disorder, disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for sommatic or germline gene therapy. The present sequence represents a dithp polynucleotide of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format
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Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mononey EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
Patury S, Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene; gene therapy; human diagnostic and therapeutic polynucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CAGCGGAGTGATGCCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATGCTATGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4277 BP; 973 A; 1253 C; 1237 G; 814 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.7%; Score 120.4; DB 13
99.2%; Pred. No. 3.4e-24;
iive 0; Mismatches 1;
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Claim 1; Page; 190pp; English.
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Matches 121; Conservative
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Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers

99US-0127958P.

06-APR-1999; UYEC-) UNIV

EAST CAROLINA.

24-MAR-2000; 2000WO-US008020

Disclosure; Page 252-254; 1592pp; English

and respiratory obstructions

WPI; 2000-679539/66.

Nyce JW; NYCE/)

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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A perform one of the 2722 sequences defined in the specification. A proposed of the invention may have a use in gene therappy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers, a dithp polynucleotide of the invention. Note: The sequence represents a dithp polynucleotide of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1348 CAGCGGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1407
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                                                                                          New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 4278;
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0; Mismatches 1; Indels
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Matches 121; Conservative
                      WPI; 2004-329368/30.
P-PSDB; ABM84191.
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The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense coligonucleotides the A is replaced by a 'Universal' or alternative base. (C) ilgonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antinflammatory, analgesic. (I) can have respiratory bronchodilator, antinflammatory, analgesic. (C) immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. (C) the antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with conting peptide factors and malignancies, such as stimulating and contingual proteins and transmitters, transcription factors, contral communoglobulins and antibodies, antibody receptors, cytokines and chemokine, endogenously produced specific and non-specific enzymes, contral chemokine receptors, adenosine receptors, bradykinin receptors, contral corvous system (CNS) and peripheral nervous and non-nervous system corresponders, CNS and peripheral nervous and non-nervous system creeptors, binding proteins and malignancy associated proteins. The receptors, binding proteins and malignancy associated proteins. The creeptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or condition and from malignancy associated with a disease or condition and from malignancy associated with a disease or condition and from malignancy associated with a disease or condition and from malignancy and proteins and malignancy associated with a disease or condition which are associated with a disease or condition which are associated minimum and malignanc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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46.7%; Score 120.4; DB
Best Local Similarity 99.2%; Pred. No. 4e-24;
Matches 121; Conservative 0; Mismatches
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Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                       Human, antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiinsthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 12386; 872pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                            Katz E,
                                                                                                                                                                                                                                                             Sandrasagra A, Ka
,, Shahabuddin S;
                                                                                                                                                                                          23-APR-2002; 2002WO-US013135.
                                                                                                                                                                                                                24-APR-2001; 2001US-0286137P.
                                                                                                                                                                                                                                     (EPIG-) EPIGENESIS PHARM INC.
                     Human nucleic acid sequence
(first entry)
                                                                                                                                                                                                                                                            Li Y, Sar
Tang L,
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                                                                                                                                               WO200285308-A2.
                                                                                                                         Homo sapiens.
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17-0CT-2003
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                                                                                                                                                                                                                                                                                                                                                      ubiquinone.
                                                                                                                                                                                                                                                                      Miller S,
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Pabalan J, Aguilar D;

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genome flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a composition a natisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine creeptor, producing bronchodilation, increasing levels of ubiquinone or lung inflammation, lung allergies, or a respiratory disease or condition, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed process or sequence data for this patent is not represented in the printed process or sequence data for this patent is not represented in the printed process or sequence data for this patent is not respiratory disease.

ö 0; Gaps Sequence 8222 BP; 1731 A; 2574 C; 2360 G; 1557 T; 0 U; 0 Other; Score 120.4; DB 10; Length 8222; 1; Indels Pred. No. 4e-24; 0; Mismatches 46.7%; Local Similarity 99.2 nes 121, Conservative Query Match Matches

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1011 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG 1070
                                            951 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010
                                                                                      61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG 120
CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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1071 CT 1072

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Human; antisense; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallergic; antiinflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vacoconstriction; respiratory distress syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; Aguilar D; Human inducible nitric oxide synthase DNA fragment 1897. pulmonary transplantation rejection; ds ABD19730 standard; DNA; 8222 BP 23-APR-2002; 2002WO-US013143. 24-APR-2001; 2001US-0286036P. (EPIG-) EPIGENESIS PHARM INC (first entry) WO200285309-A2. Homo sapiens. 29-JUL-2004 31-OCT-2002. ABD19730; RESULT 34 ABD19730

t Pharmaceutical composition for treating asthma, has antisense oligonucleotide containing less percentage of adenosine, targeted trucleic acids associated with lung airway or lung dysfunction, and bronchodilating agent.

Pabalan J,

Katz E,

s;

Sandrasagra A,

Li Y, Sar Tang L,

Miller S,

Nyce JW,

WPI; 2003-093058/08.

Claim 15; SEQ ID NO 12386; 763pp; English.

currenting adenosine sensitivity, levels or adenosine (A) or (A) receptors, curfactant depletion or hyposecretion, when administered to a mammal. The oligonucleotides are derived from a gene encoding or regulating conjugonucleotides are derived from a gene encoding or regulating conjugonucleotides are derived from a sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery or lung device, in separate containers, (b) the oligonucleotides, (c) containers, (do instructions for adding a carrier and for use of the kit. The composition of the invention has antiallergic, antiinflammatory, antiasthmatic, analgesic, hypotensive, immunosuppressive and cytostatic activity, is a beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered composition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to crackuce the amount of target polypeptide present in the lungs. The pulmonary obstruction, and/or bronchoconstriction and/or lung inflammation, allergies and/or surfactant hypoproduction are associated with, a disease or condition such as pulmonary viseostriction, contained and allergies, asthma, impeded respiration, respiratory contains at him at incompay and a second allergies, asthma, impeded respiration, respiratory contains pain, cystic fibrosis, allergic rhinitis, pulmonary contranspondence ontent of the anti-sense oligos corresponding to the reduced adenosine content of the anti-sense oligos corresponding to thymidines present in the target RNA serves to prevent the breakdown of the oligonucleotides into products that free adenosine into the system receptors, This invention describes a novel composition (a) a first active agent, comprising oligonuclectides, effective for alleviating. bronchoconstriction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptor

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1010
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                                                                                                                                    o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects affilict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
                                                                                                                                                                                                                                               GGCTACCAGATGCCAGATGGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                         9
e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, prevent any unwanted effects due to it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic, antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
                                                                                                                                                                                               951 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCTATGCT
                                                                                                                                                                     1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                  Sequence 8222 BP; 1731 A; 2574 C; 2360 G; 1557 T; 0 U; 0 Other;
                                                                                             Length 8222;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human adenosine receptor related polynucleotide SEQ ID NO:2509.
                                                                                                                                1; Indels
                                                                                 Disclosure, Page 666-669; 1343pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA34820 standard; DNA; 9513 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA34820;
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                                                                                           Query Match
Best Local
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                                                                                                                                Matches
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Fibrosis, plannary hypertension, emphysems, fironic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the calcuses side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA3233 to AAA35312 represent invention, which correspond to SEQ ID No:11 to 285, and then the last 185 sequences are also called SEQ ID No:11 to 185, but the sequences differ from the previously named sequences. SEQ ID No:11 to 1860 (AAA3233 to AAA3392) are specifically claimed ONS from the present invention. N.B. Sequences given in the disclosure of the present invention on one match with their corresponding SEQ ID NO: sequences given in the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2242 cagcggagrgarggcaagcacacrrccggrgrggaargcrcagcrcarccgcrargcr 2301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Low adenosine antisense oligonucleotide; phosphorothioate, allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiathmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                      Sequence 9513 BP; 2107 A; 2869 C; 2671 G; 1866 T; 0 U; 0 Other;
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0
                                                                                                                                                                                                                                                                                                                                                                                          46.7%; Score 120.4; DB 3; Length 9513; 99.2%; Pred. No. 4.1e-24; ive 0; Mismatches 1; Indels 0;
respiration, respiratory distress syndrome, pain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human low adenosine antisense oligonucleotide #2509.
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J W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2362 CT 2363
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                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nyce JW;
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                                                                                                                                                                                                                                                                                                                Listing
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WPI; 2000-679539/66

Homo sapiens.

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The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense coligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and certivating peptide factors and transmitters, cranscription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, chemokine receptors, adenosine receptors, cytokine and chemokine receptors, adenosine receptors and heir receptors, cransmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The receptors binding proteins and malignancy associated proteins. The receptors binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergies, asthma, impeded respiratory vasocoactiction, inflammation, allergies, asthma, impeded respiration, respiratory discress syndrome (CRDs) bronch comes in the series of an elected from pulmonary vasocoactiction, inflammation, allergies, antibors.
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                Low adenosine (A) content antisense oligonuclectides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; antisense; lung dysfunction; nasal airway dysfunction; antinflammatory steroid; ubiquinone; antinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CAGCGGAGTGATGCCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypertension, emphysema, chronic obstructive pulmonary disease (COPD)
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                                                                                                                        Disclosure; Page 737-739; 1592pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the present invention
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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nacal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention to as antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a cuse in antisense gene therapy. The composition may have a composition may naction are preventing a respiratory, lung or mallignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of or entiinflammation, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine creceptor, producing bronchodilation, increasing levels of ubiquinone or lung inflammation, lung allergies, or a respiratory disease or condition.

Conditioning the sequence data for this patent is not represented in the printed conditioning the sequence data for this patent is not repersented in the printed conditioning the sequence data for this patent is not repersented in the printed conditioning the sequence data for this patent is not repersented in the printed condition in the sequence data for this patent is not repersented in the printed condition in the sequence data for this patent is not repersented in the printed condition.
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                                                                                                                                                                                                                                                                                                                                                                               Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG
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                                                                                                                                                                                                                                                                   Pabalan J, Aguilar D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9513 BP; 2107 A; 2869 C; 2671 G; 1866 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 120.4; DB 10; Length 9513;
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99.2%; Pred. No. 4.1e-24;
Five 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 11878; 872pp; English.
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                                                                                                                                                                                                                                                                       Katz E,
                                                                                                                                                                                                                                                                                             Tang L, Shahabuddin S;
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                                                                                                                                                                                                                                                                       Sandrasagra A,
                                                                                                                                                                            24-APR-2001; 2001US-0286137P.
                                                                                                                                 23-APR-2002; 2002WO-US013135
                                                                                                                                                                                                                          (EPIG-) EPIGENESIS PHARM INC
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                                        WO200285308-A2
                                                                                 31-OCT-2002
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                                                                                                                                                                                                                                                                                             Miller S,
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Human, antisense, bronchoconstriction, allergy, hyposecretion, pain, respiratory tract inflammation, adenosine sensitivity; lung, cancer, surfactant depletion, antiallergic, antiinflammatory, antiasthmatic; analgesic, hypotensive, immunosuppressive, cytostatic, cystic fibrosis, beta-adrenergic agonist, respiratory disease; pulmonary vasoconstriction, respiratory distresses syndrome; allergic rhinitis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease; bronchitis, pulmonary transplantation rejection, ds. WO200285309-A2 Homo sapiens.

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31-OCT-2002.

23-APR-2002; 2002WO-US013143.

24-APR-2001; 2001US-0286036P.

(EPIG-) EPIGENESIS PHARM INC

Pabalan J, Aguilar Katz E, Li Y, Sandrasagra A, Ka Tang L, Shahabuddin S; Nyce JW, L Miller S,

ä

WPI; 2003-093058/08.

Pharmaceutical composition for treating asthma, has antisense obligonuclocide containing less percentage of adenosine, targeted tuncleic acids associated with lung airway or lung dysfunction, and bronchodilating agent.

Claim 15; SEQ ID NO 11893; 763pp; English.

This invention describes a novel composition (a) a first active agent, comprising oligonucleotides, effective for alleviating comprising oligonucleotides, effective for alleviating comprising oligonucleotides, readiction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The colsonucleotides are derived from a gene encoding or regulating expression of a target polypeptide associated with lung airway or lung expression of a target polypeptide associated with lung airway or lung device, in separate containers, (b) the oligonucleotides, (c) instructions for adding a carrier and for use of the kit. The composition of the invention as antiallergic, antialitammatory, antianthmater, antianthmater, antialitammatory, in an antialitation and cytostatic activity, is a beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered composition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mana or analogue present in the lungs. The pulmonary obstruction, and/or bronchoconstriction and/or lung inflammation, allergies and/or bronchoconstriction are associated inflammation, allergies asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic thinitis pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to the production and active pulmonary infections are the produced and and active pulmonary infections and active pulmonary infections the present in the target RNA serves to prevent the breakdown of the produced active to the produced

Sequence 9513 BP; 2107 A; 2869 C; 2671 G; 1866 T; 0 U; 0 Other;

free adenosine into the system

tissue environment and

the oligonucleotides into products that e.g., lung, brain, heart, kidney, etc, prevent any unwanted effects due to it

ö Query Match 46.7%; Score 120.4; DB 11; Length 9513; Best Local Similarity 99.2%; Pred. No. 4.1e-24; Matches 121; Conservative 0; Mismatches 1; Indels 0;

1 CAGCGGAGTGATGGCAAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT

2302 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG 2361 2242 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 2301 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120 Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; bund united depletion; respiratory; bronchodilator; antisfinammatory; immunosuppressive; antisthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; Human enzyme-related antisense polynucleotide #3003. AAF21436 standard; DNA; 35384 BP. (first entry) CT 2363 121 GT 122 14-MAR-2001 2362 AAF21436;

Homo sapiens.

cancer; 88

WO200062736-A2

26-OCT-2000

24-MAR-2000; 2000WO-US008020.

06-APR-1999;

(UYEC-) UNIV EAST CAROLINA. (NYCE/) NYCE J W.

Nyce JW;

WPI; 2000-679539/66.

Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions

Disclosure; Page 47-55; 1592pp; English.

oligonuclectides and compositions (I) comprising them. In the antisense oligonuclectides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antinfilammatory, analgesic, immunosuppressive, antisthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and mallghancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adenosine receptors, cytokine and chemokine receptors, adenosine receptors, bradkinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system peptide receptors, defensine, growth factors was one peptide creeptors, binding proteins and malignancy associated proteins. The receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders present invention describes low adenosine (A) content antisense

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28173 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG 28232
                                                                                                                                                                                                                                                                                                                                                                                                                                             28113 cadeddadrgarddecaadeacaetreeddargaaardereadereadearaet 28172
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and/or bronchoconstriction) and/or lung inflammation, allergy(les) and/or autactant hypoproduction which are associated with a disease or condition selected from pulmonary vasconstriction, inflammation, allergy (RDS) as the cash as a seconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAPISH34 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
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                                                                                                                                                                                                                                                                                                                                                                                                      1 CAGCGGAGTGATGCCAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                               Length 35384;
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cal Similarity 99.2%; Pred. No. 5.5e-24;
121; Conservative 0; Mismatches 1:
                                                                                                                                                                                                                            the present invention
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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ABZ97130 standard; DNA; 35459 BP.
                   Human nucleic acid sequence.
              (first entry)
              17-0CT-2003
         ABZ97130;
RESULT 40
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28233 CT 28234

Search completed: December 13, 2005, 16:32:42 Job time : 476 secs

Human, antisense; lung dysfunction; nasal airway dysfunction; antinflammatory steroid; ubiquinone; antinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodiation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

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23-APR-2002; 2002WO-US013135.
                                                                                                                                                    24-APR-2001; 2001US-0286137P.
                                    WO200285308-A2
Homo sapiens
                                                                          31-OCT-2002
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Pabalan J, Aguilar D; Sandrasagra A, Katz E, L, Shahabuddin S; Li Y, San Tang L, Miller S, Nyce JW,

(EPIG-) EPIGENESIS PHARM INC

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

SEQ ID NO 12372; 872pp; English. Disclosure; The invention relates to a novel pharmaceutical composition, which has

first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, cimmunosuppressive, and cytostatic activity. The composition may have a cuse in antisense gene therapy. The composition is useful for treating or preventing a respiratory lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing levels of adenosine or receptor, producing bronchodilation, increasing levels of adenosine creceptor, producing bronchodilation, increasing levels of adenosine creceptor, producing bronchodilation, increasing levels of ubiquinone or lung inflammation, lung allergies, or a respiratory disease or condition. Once: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO 28248 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 28307 28247 9 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT Gaps Sequence 35459 BP; 7025 A; 10160 C; 10041 G; 7897 T; 0 U; 336 Other; DB 10; Length 35459; ö Indels Score 120.4; DB 10; Pred. No. 5.5e-24; at ftp.wipo.int/pub/published_pct_sequences 0; Mismatches 46.78; Matches 121; Conservative Local Similarity 28308 CT 28309 GT 122 Н 121 Query Match ò 임 ò 셤 ò 셤

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AK077896 Mus muscu CE744130 UI-M-CV0-CX385985 JGI XZT65 BP178167 BP178167 AZ044226 RPCI-23-3 DQ045247 Homo sapi BJ088070 BJ088070 AL125658 Fugu rubr DQ045248 Pan trog1 CK016997 AGENCOURT BU425320 603961089 DR123141 49091370 DN757217 GL-CF-140 AJ334075 AJ394075 CK459880 UI-M-HB0-BJ733387 BJ733387 AL053013 Drosophil CA090625 SCSGAMZ10 CCS70671 AGENCOURT AK185276 Mus muscu BX919466 BX919466

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Searched:

Database

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טטפ-JUN-2005 DNA linear GSS 02-JUN-2005
Homo sapiens NOS2A gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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I (bases 1 to 2994)

Nielsen, K., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,

Hubisz, M.J., Fladel-Alon, A., Tanenbaum, D.M., Civello, D.,

White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.

A can for Positively Selected Genes in the Genomes of Humans and

Chimpanzees

(er) PLoS Biol. 3 (6), E170 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 2994)
Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B. Mielsen, R., Bustamante, C., Tanenbaum, D.M., Civello, D., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of
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Best Local Similarity 99.2%; Pred. No. 6.7e-21;
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AUTHORS
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AW65410 103369 MA
AQ800595 HS_5314_B
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AY419784 Homo sapi
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AY419786 MMS muscu
BC083183 MMS muscu
BC06101 MMS muscu
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                         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                   41078325 seqs, 23393541228 residues
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FR0038175
AQ331351
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Homo sapiens
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Pan troglodytes NOS2A gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
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                   GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                 805 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hominidae, Pan.

I (bases 1 to 2994)

Nielsen, F., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
Hubisz, M.J., Fladel-Alon, A., Tanenbaum, D.M., Civello, D.,
White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.

A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees

Chimpanzees
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Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civello, D., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA.
This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              805 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG
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    .2994
    /organism="Pan troglodytes"
/mol_type="genomic DNA"
    /db_xref="taxon:9598"

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/gene="NOS2A"
/locus_tag="HC15370"
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Pan troglodytes
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AQ214630
HS_3117_A1_F08_T7 CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3117 Col=15 Row=K, genomic survey
                                                                                                                                                                                                                                                                                                                   Hominidae; Homo.
1 (Bases 1 to 453)
Mahairas G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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[ tbase 1 to 553]
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
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103369 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
AW654110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109,
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
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/db_xref="taxon:9606"
/clone="Plate=3117 Col=15 Row=K"
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Plate: 3117 row: K column: 15
Class: BAC ends
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Location/Qualifiers
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GSS.
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                                                                                                                                                                                                      Homo sapiens (human)
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AUTHORS
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Jniversity of Washington
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1 (bases 1 to 523)
Mahairas, G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                           USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4360
Email: smith@email.marc.usda.gov
Emails sequencing. Bases called and alt_trimmed with phred
9109194.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
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High Throughput Sequencing Center
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Pred. No. 8.5e-17;
0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Bos taurus"
/mol type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="MARC 1BOV"
                                                                                                                                                                                                                                                                                                               BACKWARD: GTTTTCCCAGTCACGACG
Plate: 95 rows. L column:
Seq primer: ATTTACGTGACTATAG.
Location/Qualifiers
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FORWARD: AGGAAACAGCTATGACCAT
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Homo sapiens
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Hominidae; Homo.
1 (bases 1 to 518)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Mahairas,G.G., Wallace,J.C., Smith,X., Zhao,S., Adams,M.D. and
Hood,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
/clone lib="RPCI-11 Human Male BAC Library"
/clone lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
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HS 5542 Bl H02 T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic_clone Plate=1118 Col=3 Row=P, genomic survey sequence.
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101 Queen Ann Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Eax: (206) 616-3618
Email: jwallace300. Washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please context Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Place: 890 row: H column: 2
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109,
Tel: (206) 616-3618
Fax: (206) 616-3618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="Plate=890 Col=2 Row=H"
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/organism="Homo gapieng"
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High quality sequence stop: 523.
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E 1 (bases 1 to 842)
S Holt,R.; Stott,J.; Yang,G.; Barber,S.; Smailus,D.; Prabhu,A.-L., Radi,M.; Cloutier,A.; Lee,D.; Girn,N.; Olson,T.; Mayo,M.; Butterfield,Y.; Kirkpatrick,R.; Liu,J.; Girn,R.; Ghan,A.; Chiu,R.; Mathewson,C.; Wye,N.; Masson,A.; Brown-John,M.; Jones,S.; Schein,J.; Marra,M.; de Jong,P.; McWilliam,S.; Barris,W.; Dalrymple,B.P. and Tellam,R.

E Bovine BAC End Sequences from Library CHORI-240; PLATES 294 to 398 to Unpublished (2003)
Contact: Rob Holt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing the British Columbia Cancer Agency Genome Science Centre 600 W 10th Ave, Vancouver, British Columbia, Canada V52 4E6 Tel: 604-877-6085

Fax: 604-877-6085

Email: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Piecer de Jong (pdejong@mail.cho.org). Clones may be purchased from BACRAR Resources
(http://www.chori.org/bacpac/ordering_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
                                                                                                                                                                                                                                                                                                                                                  /clone_lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
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CH240 367118.T7 CHORI-240 Bos taurus genomic clone CH240_367118, genomic survey sequence.
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(pieter@dejong.med.buffalo.edu). Clones may be purchased from ABCPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server:
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                                                                                                                                                                                                                                                             /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="Plate=1118 Col=3 Row=P"
                                                                                                                                                                                                                                        organism="Homo sapiens"
                                                                                           Plate: 1118 row: P column: 3
Seg primer: T7
Class: BAC ends
High quality sequence stop: 518.
Location/Qualifiers
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CC520102.1 GI:31838390
                                                                                                                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96; Conservative
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Matches 96; Conserv
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SOURCE
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                                                                                                                                                                                          FEATURES
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence as made by sequencing genomic exons and ordering them
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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1 (bases 1 to 3437)

1 (Lark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                            /cell_type="Blood"
/clone_lib="CHORL-240"
/note="Vector: pTARBACL.3; Site_l: Mbol; Site_2: Mbol;
Harreford bull il Domino 99375; CHORL-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       471 CAGAGGACCGACGACACGACTTCCGCGTTTGGAACTCCCAACTCATCGCTACGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gape
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Homo sapiens NOS1 gene, VIRTUAL TRANSCRIPT, partial sequence,
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 842;
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Columbia Genome Sciences Centre, Canada.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 90.2; DB 9;
Pred. No. 4.9e-13;
0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 302 (5652), 1960-1963 (2003)
                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_367118"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                                                 Location/Qualifiers
1. .842
/organism="Bos taurus"
                         column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GTACCCGGCCCAGCCTCAGCCRC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      591 GTAGGCGCCCCCCCTCCCC 613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genomic survey sequence. AY419784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 35.0%;
Best Local Similarity 76.9%;
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                          /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
                      Plate: 367 row: I
Seg primer: T7
Class: BAC ends.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Miroidea; Murinae; Mus. Sciurognathi; Miroidea; Murinae; Mus. 1 (bases 1 to 526) and to 526) and to 526; Edwards, J. Finch, R. Piggott, J., BeltrandenRio, Hu, Y., Richter, L. J., Fridle, C. J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Rey, B. W. Jr., Kipp, P., Kohlhauff, B., Ma, Z. -O., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z. -Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N. Zu, O., Person, C. and Sands, A.T. Wogel, P., Walke, W., Xu, N. Zu, O., Person, C. and Sands, A.T. Wogel, P., Walke, W., Zu, C., Change, C., Cand, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                CG506126 526 bp mRNA linear GSS 01-OCT-2003
OST55467 Mus musculus 1298v/Ev Mus musculus cDNA clone OST55467,
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                                                            64 Gectacaagcagccagarggcrcraccrrggggarccagcraargrggagrfcacaga 123
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           GGCTACCAGATGCCAGATGGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG
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4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
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Pred. No. 1.2e-09;
0; Mismatches 28; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="OST55467"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="129Sv/Ev"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:37284915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Zambrowicz BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.9%;
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                                                                                                                                                                                                                                                                                                                                                                             nRNA sequence.
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                                                                                                                         121 GT 122
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                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                   DEFINITION
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                  RESULT 10
CG506126
                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
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Zambrowicz, B. P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., BeltrandelRio, H., Buxton, B.C., Edwards, J., Finch, R.A.,
Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
Friddle, C.J., Gupter, P., Kohlhautf, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Sparks, M.J., van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.
Zhu, Q., Person, C. and Sands, A.T.
Whit Kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
                                                                                                                                                                                                                                                                                                                                                      61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                            9
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
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0
                                                                                                                            Length 3437;
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/clone_lib="Mus musculus 129Sv/Ev"
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                                                                                                                       Score 78.2; DB 10;
Pred. No. 8.7e-10;
0; Mismatches 28;
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    .486
    /organism="Mus musculus"

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/strain="129Sv/Ev"
/db_xref="taxon:10090"
                 /gene="NOS1"
/locus_tag="HCM7006"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                               Query Match 30.3%;
Best Local Similarity 77.2%;
Matches 95; Conservative
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Matches 94; Conservative
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Email: cgapbe-rape control of the control of lower Tissue Procurement: Dr. James Lin, University of Iowa Tissue Procurement: Dr. James Lin, University of Iowa CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing Dy: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Maryland; Contact: nisc. magosmhgri.nih.gov/Contact: nisc. magosmhgri.nih.gov/Contact: nisc. magosmhgri.nih.gov/Akhter.N., Ayele.K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakeley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks.S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soarea, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J. Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.J., Mullak, S.J., Bosak, S.A., McEwan, P.J., Morley, K.C., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, V.I. Halton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Youchman, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Youchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schwutz, J., Myers, R. Schnerch, A., Schein, J.E., Gromes, S.J. and Marra, M.A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1860 CAAAGGACTGATGGCAAGCATGCATCCGAGTGTGGAACTCGCAGCTCATCCGCTATGCC 1919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 176 Row: o Column: 2 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6724320 This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (24-SEP-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
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/lab_host="DH10B"
/note="Vector: pYX-ASC"
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/organism="Mus musculus"
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/clone="IMAGE:30533636"
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/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: MGC help desk
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     AY419786 3420 bp DNA linear GSS 17-DEC-2003
Mus musculus NOS1 gene, VIRTUAL TRANSCRIPT, partial sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence as made by sequencing genomic exons and ordering them
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.
                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Giurognathi, Muroidea, Murinae, Mus.

1 (bases 1 to 3420)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Tanenbaum, D.M., Civello, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
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Pred. No. 1.6e-09;
0; Mismatches 28
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/locus_tag="HCM7006"
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Location/Qualifiers
                                                                                                                                                                          Mus musculus (house mouse)
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                                                                   genomic survey sequence.
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1 Similarity 77.0%;
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DEFINITION

RESULT 13 BC066101

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ORGANISM

VERSION KEYWORDS SOURCE

ACCESSION

REFERENCE AUTHORS

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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence as made by sequencing genomic exons and ordering them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AY419785 3430 bp DNA linear GSS 17-DEC-2003 Pan troglodytes NOS1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
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L bases 1 to 3430)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Territera, S., Wango, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, White, T.J., Sninsky, J.J.,
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG
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0
                                                                                                                                                                                                                                                                                                                                                                                                               Length 5626;
This clone has the following problem: frame shifted.
Location/Qualifiers
1. .5626
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         29.9%; Score 77.2; DB 4; 77.0%; Pred. No. 1.7e-09; tive 0; Mismatches 28;
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
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                                                                                                                                                                           /db_xref="taxon:10090"
/clone="IMAGE:30533636"
/tisue_type="Brain"
/clone_lib="NIH BMAP_GIO"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                           /note="Vector: pYX-ASC"
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Location/Qualifiers
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Pan troglodytes
                                                                                                                        /mol_type="mRNA"
/strain="C578L/6"
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Matches 94; Conserv
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CE 1 (bases 1 to 5626)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Schuler, G.B., Klausner, R.D., Collins, F.S., Wagner, L., Schemmen, C.M., Schuler, G.D., Alteschul, S.F., Zeeberg, B. Buetow, K.H., Schemer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casarant, F.J., Scheetz, T.E., Brownstein, M.B., Bonaldo, M.F., Casarant, F.J., Scheetz, T.E., Brownstein, M.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6724320
                                                                                                                                                                                                                                                                                                                                                   Mus musculus nitric oxide synthase 1, neuronal, mRNA (cDNA clone IMAGE:30533636), containing frame-shift errors.
                                                                              1920 GGCTACAAGCCAGATGGCTCTACCTTGGGCGATCCAGCTAATGTGGAGTTCACAAG 1979
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Whe fatte: http://genome.uiowa.edu
Contact: bento:soareeGuiowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,
Bishlar,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WIH-WGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
                                          61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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Submitted (02-PEB-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human and mouse CDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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Mus musculus
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PUBMED REFERENCE AUTHORS TITLE JOURNAL

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Contact: Simon Hubbard
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Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea, Murinae; Mus.

E 1 (bases 1 to 540)
S Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Fligott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Friddle, C.J., Gupta, A., Hannsen, G., Hu, Y., Huang, W., Jaing, C.,
Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Sparks, M.J., van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.
Whil kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
D 14610273
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                                                                                                                                                                                                                                                                               CG650955 540 bp mRNA linear GSS 02-OCT-2003 OST410927 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST410927,
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Location/Qualifiers
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4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
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Score 76.8; DB 10; Length 3430;
Pred. No. 2e-09;
0; Mismatches 27; Indels 0;
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-clone="0587410927"
|cell type="embryonic stem cell"
|clone_lib="Num musculus 1295v/Ev"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="mRNA"
/strain="1295v/Ev"
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CG650955
CG650955.1 GI:37474804
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Query Match
Best Local Similarity 77.5%;
Matches 93; Conservative
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1 (bases 1 to 892)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A. Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
820 bp mRNA linear EST 07-AUG-2003
hdm005_c06 LPS-activated macrophage cell line Gallus gallus cDNA,
CP251860
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603151629F1 CSEQCHL19 Gallus gallus cDNA clone ChEST15918 5', mRNA
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                                                                                                                                                                                                         Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
I (bases I to 820)
Wittzell, H., Bed'Hom, B., Morin, V., Young, J.R., Whittaker, C.J.,
Chausse, A.M. and Zoorob, R.
Unpublished (2003)
Contact: Zoorob R
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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/db_xref="taxon:9031"
/coll_line="HD11"
/cloe="loe"lib="LPS-activated macrophage cell line"
/note="Vector: pTriplEX2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .820
/organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 rue Guy Moquet, BP 8, 94801
Tel: 33 1 49 58 35 00
Fax: 33 1 49 58 33 81
Email: coorob@vjf.cnre.fr.
Location/Qualifiers
                                                                                                                                                           CF251860.1 GI:33485115
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Gallus gallus
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621 bp DNA linear GSS 14-JUN-2000
Mus musculus genomic clone RPCI-23-82G23,
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Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 1SB. UK Email: biohelp@dmgn.mrc.ac.uk Vector: pBluescript II KS
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 28.2%; Score 72.8; DB 11
1 Similarity 74.2%; Pred. No. 1.8e-08;
92; Conservative 0; Mismatches 32
                                                                                                                                                                                                                                                                                           1. .581
/organism="Takifugu rubripes"
                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic_DNA"
/db_xref="taxon:31033"
/clone="064007cF12"
/clone_lib="cosmid_064007"
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="CSEQCHL19"
/note="Organ: liver; Vector: pBluescript II KS(+); Site 1:
EcoRI; Site 2: Not!; Modification of pBluescript II KS(+)
[Stratagene] vector to accommodate cDNA produced with the
T-trimmed protocol (Construction of uni-directionally
cloned cDNA libraries from messenger RNA for improved 3'
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
Ligate in double stranded adaptor containing BsgI and
BamHI sites [5'ggcggggaggccggagccggatcggaaaaaaaag]
[5'aattcttttttcggatccgggatcgaagccggl"]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blgar,G., Clark,M.S., Smith,S., Meek,S., Warner,S., Edwards,Y.J.K.,
Umrania,Y., Williams,G. and Brenner,S.
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Fugu rubripes GSS sequence, clone 064007cF12, genomic survey
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Bouchireb, N., Cottage, A., Yeo, G.S., Umrania, Y., Williams, G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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                 of Biomolecular Sciences of Manchester Institute of Science and Technology
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ilarity 75.4%; Pred. No. 9.1e-
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="ChEST15918"
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Genome Res. 9 (10), 960-971 (1999)
                                                                                                  PO Box 88, Manchester, M60 1QD, UK
                                                                                                                                                                                                                                          1. .892
/organism="Gallus gallus"
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GSS; genome survey sequence.
Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
                                                                                                                            Tel: 01612008930
Fax: 01612360409
Email: Simon Hubbard@unist.ac.uk.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         /sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 581)
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Matches 92; Conserv
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                    Department
University
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FR0038163
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Hominidae; Homo.

1 (bases 1 to 470)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ095690 470 bp DNA linear GSS 27-AUG-1998 HS 3017 Al F08 MR CIT Approved Human Genomic Sperm Library D Homo Bapiens genomic clone Plate=3017 Col=15 Row=K, genomic survey
                                                                                                                                                                                                                                                                                                      GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                 320 GGGNACAAACAGCCTGATGGTCAGATCNTGGGGGACCCTGCTAATGTTGAATTTANTGAG 261
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="CIT_Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                                                                                                                                                                                                                                        cceaceacacacaacaacareactrirceacierecaacacicaeciearircerratecr
                                                                                                                                                                                                          1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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                                                                                                                                                                 Gарв
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
                                                                                                              Length 581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h Similarity 98.6%; Pred. No. 4.5e-07; Similarity 98.6%; Pred. No. 4.5e-07; 68; Conservative 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                               Indels
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109,
Tel: (206) 616-3818
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                 35;
                                                                                                                   DB 11;
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                                                                                                              Score 69.8; DB 11
Pred. No. 1.1e-07;
0; Mismatches 35
                     /clone="064007cE10"
/clone_lib="cosmid 064007"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic_DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 470.
/db_xref="taxon:31033"
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AQ095690.1 GI:3463425
                                                                                                                 Query Match
Best Local Similarity 71.8%;
Matches 89; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
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Class: BAC ends
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Best Local (
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AQ095690/c
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                                                                                                          /Bexa"Female"
/lab host="DH10B"
/clone_lib="RPCI-23"
/clone_lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of ECORI and ECORI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Generation and analysis of 25 Mb of genomic DNA from the pufferfish Fugu rubripes by sequence scanning Genome Res. 9 (10), 960-971 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FR0038175 581 bp DNA linear GSS 25-FEB-2004 Fugu rubripes GSS sequence, clone 064007cE10, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 581)
Bgar,G. Clark,M.S., Smith,S., Meek,S., Warner,S., Edwards,Y.J.K.,
Umrania,Y., Williams,G. and Brenner,S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAACGTGGAATTCACTCAGGTACCCGGCCCAGCCTCAGCCRCCGGCCATTGGGGGCGGGG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCACCTTGGAGTTCACCCAGGTA-CTGACTCAGCCTCTCCTAGATCCCTGTGGGCAGGGG 119
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Atinopteryydii, Neopteryyli, Taleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (11-0CT-1999) MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 1SB. UK Email: biohelp@hgmp.mrc.ac.uk biohelp@hgmp.mrc.ac.uk Vetor: pBluescript II KS V type: PAgemid PRIMER: KS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CACAGCTCATCCGGTACGCTGGCTACCAGATGCCCGATGGCACCATCAGAGGGGATGCTG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 CTCAGCTCATCCGCTATGCTGCCTACCAGATGCCAGATGGCAGCCATCAGAGGGGACCCTG
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                                                                                                                                                                                                                                                                                                                                                                                             Score 70; DB 9; I
Pred. No. 9.7e-08;
1; Mismatches 26;
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL125676.1 GI:6107291
SGS; genome survey sequence.
Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
organism="Mus musculus"
                     /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-82G23"
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FR0038175/c
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셤 ò 요 ò 셤

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In Manages I. (Mage. nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov

This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                                            лизоват EST 14-MAR-2002
UI-M-EHOp-buu-d-15-0-UI.r1 NIH BMAP_EHOp Mus musculus cDNA clone
IMAGE:5687006 5', mRNA sequence.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGTATGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                       Mus musculus (house mouse)
Mus musculus
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Matches 86; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
Email: cdnadgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details.
Plate: H4012 row: E column: 11
Seq primer: -21M13 Reverse
High quality sequence stop: 520
POLYA=No.
                                                                                                                                                                                                                                            H4012E11-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone H4012E11 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 520)
VanBuren,V., Piao,Y., Dudekula,D.B., Qian,Y., Carter,M.G.,
Martin,P.R., Stagg,C.A., Bassey,U., Alba,K., Hamatani,T.,
Kargul,G.J., Luo,A.G., Kelso,J., Hide,W. and Ko,M.S.H.
Assembly, verification, and initial annotation of NIA 7.4K mouse
CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGATATGCT
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Pred. No. 2.8e-06;
0; Mismatches 36;
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|db xref="taxon:10090"
|clone="H4012E11"
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Genome Res. 12 (12), 1999-2003 (2002)

    .520
    /organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL/6"

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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
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Contact: Yong Qian
Laboratory of Genetics
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70.5%;
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86; Conservative
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                                                                                            GGCTACCAG 1
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                                            LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db xref="taxon:10090"
/clone="INAGE:30662039"
/clone="INAGE:30662039"
/tissue_type="Upper Head"
/dev stage="embryo 9.5 - 10.5 dpc"
/db host="Byllow (T1 phage resistant)"
/clone=lib="MINH BMAP HOO"
/note="Organ: Upper Head; Vector: pYX-Asc; Site_1: ECOR I; Site_2: Not I; The library was constructed according Bonafo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarcse gel First strand CDNA synthesis was primed with oligo-dT primer containing a Not I site .Double strand CDNA was size selected according to mRNA size fraction, ligated with ECOR I adaptor, digested with Not! and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAACTGAAT. This library kas created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."
                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.

1. (Massea I to 843)

NIH-MCC http://mgc.nci.nlh.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-romail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa cDNA hibrary preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing Dy: Dr. M. Bento Soares, University of Iowa DNA Sequencing Dy: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousefl.html

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
                                                        CNS27461
UI-M-HQO-cpd-e-24-0-UI.rl NIH BMAP_HQO Mus musculus cDNA clone
MMGE:30662039 5', mRNA sequence.
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Location/Qualifiers
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/strain="C57BL/6"
                                                                                                                                                                                                    Mus musculus (house mouse)
                                                                                                                                                       CN527461.1 GI:46855617
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/tissue type="whole brain"
/dev stage="1,5, and 15 days newborn"
/dev stage="1,5, and 15 days newborn"
/dob hote="While III phage resistant)"
/done lib="NIH BMAP GVO"
/done lib library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand CDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand CDNA was
size selected according to mRNA size fraction, ligated with
ECOR I adaptor, digested with NotI and then cloned
directionally into pYX-Aso vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
lows Brain Anatomy Project (BMAP): "Gene Discovery in the
Developing Mouse Nervous System", supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CX385985 544 bp mRNA linear EST 05-JAN-2005
JGI XZT65278.fwd NIH XGC_tropTad5 Xenopus tropicalis cDNA clone
IMAGE:7639850 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-remail.nib.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.ulowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/clone="IMAGE:30620991"
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/strain="C57BL/6"
                                 Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: pYX-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . .660
                                                                      Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IEIKGLOPADMILVFGCRCSOLDHLYRDEVLDAQORGVFGQVLTAFSRDPGSPKTYVQ
DLLRTELAAEVHRVLCLEQGHMFVCGDVTMATSVLQTVQRILATEGGMELDEAGDVIG
VLRDQQRYHEDI FGLTLRTQEVTSRIRTQSFSLQERQLRGAVPWSFDPPGPEIPGS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue type="testis"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="13 days embryo"
22. _3630
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EQFPSVALPAPLILTQLPLLQPRYYSVSSAPSAHPGEIHLTIAVLAYRTQDGLGPLHY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="unnamed protein product; nitric oxide synthase 3, endothelial cell (MGD|MGI:97362, GB|NM_008713, evidence: BLASTN, 99%, match=3633)
                                         Division of Experimental Animal Research in Riken contributed to
   Center and Genome Science Laboratory in RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                          prepare mouse tissues.
Please visit our web site for further details.
URL:http://ganome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol type="mRNA"
/db strain=GSTBL/GJ"
/db xref="FANTOM DB:6030422B05"
/db xref="taxon:10090"
/clone="6030422B05"
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Gaps ö

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

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Concerne Research Group
National Institute of Agrobiological Sciences
Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan
Tel: 81-29-838-6121
Exar: 81-29-838-6121
Email: kmita@nias.affrc.go.jp
method:uni-directional, sequence direction:sequenced from T3 primer
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RPCI-23-368AS.TV RPCI-23 Mus musculus genomic clone RPCI-23-368AS,
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                                                                                    Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta, Pterygota,
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysla;
Bombycoidea, Bombycidae; Bombyx.

    (bases 1 to 721)
    (bases 1 to 721)
    (mimada,T., Okano,K. and Maeda,S.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Malpighian tubule"
/dev_stage="5th instar larva day 3"
/clone_lib="maV3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Bombyx mori"
                                          Bombyx mori (domestic silkworm)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:7091"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="maV30763"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="p50"
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                                                                                                                                                                                                        Bombyx mori cDNA
Unpublished (2000)
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.

Xenopodinae; Xenopus; Silurana.

Richardson, P., Lucas, S., Rokhsar, D., Detter, J.C., Ng, D.C., Brokstein, P. and Lindquist, E.A.

BOG Joint Genome Institute Xenopus tropicalis EST project
Unpublished (2004)

Contact: Lindquist, E.A., Richardson, P.

DoB Joint Genome Institute

2800 Mitchell Drive, Walnut Creek, CA 94598, USA

Tel: 925 296 500

Fax: 925 296 500

Email: cdn@jij-psf.org

Tissue Procurement: Richard M. Harland Laboratory, University of

California, Berkeley; http://tropicalis.berkeley.edu/home

CDNA Library Preparation: Richard M. Harland Laboratory, University
of California, Berkeley

DNA Sequencing: DoB Joint Genome Institute: http://www.jgi.doe.gov

Clone Distribution: L.M.A.G.E. Consortium/LLNL:

http://image.llnl.gov

Naming Conventions: EST name is generated by the concatenation of

the UGI Clone Id and the direction of sequencing. The suffix '.fwd'

indicates a forward sequencing read of the insert.

Small Insert: Based upon one or more sequencing reads of this clone

where vector sequence was present at both ends, this clone has been

determined to contain a cDNA insert on the order of 600-1000 bases.

High quality sequence stop: 544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NIH_XGC_tropTad5"
//note="Vector: pCs108; Site_1: Sal1; Site_2: Not1; Tadpole library constructed by Russell B. Fletcher in R. Harland's lab using poly A RNA and oligo dT primers (Invitrogen Superscript Plasmid System for cDNA Synthesis and Cloning). Salt [5, end) -Not1 (3' end) cDNA was inserted into vector pCs108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP178167

721 bp mRNA linear EST 10-OCT-2003
BP178167 maV3 Bombyx mori cDNA clone maV30763, mRNA sequence.
BP178167.1 GI:37648895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 GGATACAAACAGCCTGATGGCTCAGTGCTGGGAGACCCTGCAAATGTAGAATTGACAGAG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:7639850"
/tissue_type="whole embryo"
/de_stage="radpole (st. 36-41)"
/lab hose="E. coli Xbl-Blue derivative, Stratagene
ElectroTen-Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.7%; Score 61.2; DB 8; Length 544; 68.9%; Pred. No. 2e-05; ive 0; Mismatches 38; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Xenopus tropicalis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mol_type="mRNA"
db_xref="taxon:8364"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AT 421
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ACCESSION
VERSION
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source

FEATURES

RESULT 28 BP178167

LOCUS

Matches

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ORIGIN

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Gaps

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BJ088070 625 bp mRNA linear EST 29-SEP-2003 BJ088070 NIBB Mochii normalized Kenopus tailbud library Kenopus laevis cDNA clone XL091118 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Exa: 81-559-81-6855
Emall: tshini@genes.nig.ac.jp
The information of this clone is available through the following
                                                                                                                                                                                                                                                                                                                                                        1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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/dev stage="stage 25"
/clone_lib="NIBB Mochii normalized Xenopus tailbud
library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 625)
Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                  Score 54.8; DB 11; Length 3612; Pred. No. 0.0013;
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                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                  42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center For Genetic Resource Information
National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expressed genes in X. laevis embryo Unpublished (2001)
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Xenopus laevis"
                                      1. .3612
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL091118"
                                                                                                                                                      http://xenopus.nibb.ac.jp.
Location/Qualifiers
                   location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BJ088070.1 GI:17585186
                                                                                                                                                                                                                                                                  ch 21.2%;
1 Similarity 65.6%;
80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 19.1
Best Local Similarity 68.7
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis
alignment
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Best Local
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JOURNAL
COMMENT
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BJ088070
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KEYWORDS
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                     FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="RECI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSS 02-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 TGGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCA 119
                Email: szhadetigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pieteredejong med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 368 row: A column: 5
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae; Homo.

1 (bases 1 to 3612)

Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Fledel-A.D., Tanenbaum, D.M., Civello, D., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sackton, T.B.,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Observed to 3612)

Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B. Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B. White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission

Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DQ045247 3612 bp DNA linear GSS 02-JUJ
Homo gapiens NOS3 gene, VIRTUAL TRANSCRIPT, partial sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.2%; Score 54.8; DB 9; Length 286; 75.2%; Pred. No. 0.00086; ive 1; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 GGTACCCGGCCCCAGCCTCAGCCRCCGGCCATTGGGGCCGGGGAGCC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTA-CTGACTCTGCTGAGATCCCTGTGGGCAGGGACCC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLoS Biol. 3 (6), E170 (2005)
                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                      /db xref="taxon:10090"
/clone="RPCI-23-368A5"
                                                                                                                                                                                                                                            Location/Qualifiers
1. .286
                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic survey sequence. DQ045247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DQ045247.1 GI:66896462
                                                                                                                                                                                                                                                                                                                                                                                                                    'sex="Female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimpanzees
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KEYWORDS
SOURCE
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DQ045247
LOCUS
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AUTHORS
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AUTHORS
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JOURNAL
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Sackton, T.B.,

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii, Neoperygii; Teleostei; Ostariophysi; Cyprinidae; Danio.

1 (Dases 1 to 906)

1 (Dases 1 to 906)

1 Unpublished (1999)

1 Unpublished (1999)

1 Contact: Daniela S. Gerhard, Ph.D.

2 Office of Cancer Genomics

3 Mational Cancer Institute / NIH

4 Mational Cancer Institute / NIH

5 Mational Cancer Institute / NIH

6 Mational Cancer Institute / NIH

7 Mational Cancer Institute / NIH

8 Mational Cancer Institute / NIH

9 Mational Cancer Institute / NIH

9 Mational Cancer Institute / NIH

9 Mational
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                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae, Pan.

1 (bases 1 to 3449)
Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Flaedel-Alon, A., Tanenbum, D.M., Civello, D., White, T.J., Sainsky, J.J., Adams, M.D. and Cargill, M.

A Scan for Positively Selected Genes in the Genomes of Humans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 3449)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submissein
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCTACCGGCAGCAGGACGGCTCTGTGCGGGGGGACCCAGCCAACG 644
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Pred. No. 0.16;
0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                              PLoS Biol. 3 (6), E170 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="NOS3"
/locus_tag="HC11004"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                troglodytes (chimpanzee)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CK016997.1 GI:38542516
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Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.1%;
ilarity 65.1%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <1. . >3449
                                                              Pan troglodytes
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Best Local Similarity
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                             SOURCE
ORGANISM
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KEYWORDS
SOURCE
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CK016997
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Blgars 1 to 619)
Elgar, G., Clark, M.S., Smith, S., Meek, S., Warner, S., Edwards, Y.J.K.,
Umrania, Y., Williams, G. and Brenner, S.
Direct Submission
Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource
                                                                                                                                                                                                                                                                                                                   GSS 25-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Generation and analysis of 25 Mb of genomic DNA from the pufferfish
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Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
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Bouchireb,N., Cottage,A., Yeo,G.S., Umrania,Y., Williams,G. and
                                         CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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                                                                                                                                                                                                                                                                                                 rkuUJ8157 619 bp DNA linear GSS 25-.
Fugu rubripes GSS sequence, clone 064007cF6, genomic survey
sequence.
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                                                                                                                GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCT
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/mol_type="genomic DNA"
/db_xref="taxon:31033"
/clone="664007cpf"
/clone_lib="cosmid 064007"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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Genome Res. 9 (10), 960-971 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                           AL125658.1 GI:6107273
GSS; genome survey sequence.
Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
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biohelp@hgmp.mrc.ac.uk
Vector: pBluescript II KS
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PRIMER: KS
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Matches 60; Conserv
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FR0038157
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FEATURES

ORIGIN

RESULT 33 DQ045248

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Drosophila pseudoobscura

Drosophila pseudoobscura

Eukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;

Robytera; Endoacphilidae; Drosophila.

Ephydroidea; Drosophilidae; Drosophila.

Ephydroidea; Drosophilidae; Drosophila.

Est Chards, S., Liu, Y., Bettencourt, B.R., Hradecky, P., Letovsky, S.,

Richards, S., Liu, Y., Bettencourt, B.R., Hradecky, P., Letovsky, S.,

Nielsen, R., Thornton, K., Hubisz, M.J., Chen, R., Maisel, R.P.,

Couronne, O., Hua, S., Smith, M.A., Schroeder, S., Sodergren, E.,

Matchews, B.B., Crosby, M.A., Schroeder, A.J., Ortiz-Barrientos, D.,

Rives, C.M., Metzker, M.L., Muzny, D.M., Scott, G., Steffen, D.,

Rives, C.M., Metzker, M.B., Miner, G., Hamilton, C., Huang, Y.,

Wheeler, D.A., Worley, K.C., Havlak, P., Durbin, K.J., Egan, A.,

Galla, R., Hume, J., Morgan, M.B., Miner, G., Hamilton, C., Huang, Y.,

Waldron, L., Verduzco, D., Clerc-Blankenburg, K.P., Dubchak, I.,

Roor, M.A., Anderson, W., White, K.P., Clark, A.G., Schaeffer, S.W.,

Genbart, W., Weinstcok, G.M. and Gibbs, R.A.

Comparative genome sequencing of Drosophila pseudoobscura:

chromosomal, gene, and cis-element evolution
                                                                                                         /done liberCEEQREBNO9"
//done liberCEEQREBNO9"
//done liberCEEQREBNO9"
//done liberCEEQREBNO9"
Site 2: Not1; This normalized library was constructed from Site 2: Not1; This normalized library was constructed from site 2: Not1; This normalized library was constructed from lamilion independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to Not1 adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DR123141
49091370 Drosophila pseudoobscura embryonic cDNA library Drosophila
pseudoobscura cDNA clone K7 5', mRNA sequence.
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/tissue_type="Chondrocytes isolated from growth plate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.7%; Score 43.2; DB 5; Length 688; 75.0%; Pred. No. 1.1; cive 0; Mismatches 18; Indels
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Baylor College of Medicine
One Baylor Plaza, Houston, TX 77030, USA
Tel: 713-798-6667
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NCB1 Trace Archive: 226697760
Insert Length: 1750 Std Error: 0.25.
Location/Qualifiers
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Contact: Stephen Richards
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Matches 54; Conserv
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DR123141
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                                                                                                                                                                                                                                                                                       /clone="Intage:704444"
/clone="Intage:704444"
/tissue_type="whole body"
/lab host="DH108"
/clone lib="WHH ZGC 10"
/clone lib="WHH ZGC 10"
/clone lib="WHH ZGC 10"
/clone lib="Whot is zerolected from a whole adult individual
from the Tuebingen strain. is strand cDNA was primed with
a Not I - oligo(dT) primer, double-stranded cDNA was
cloned into the Not I and EcoRV sites of pExpress-1.
Library was size-selected for >1 kb fragments. A
normalized version of this library is also available
(NIH ZGC 7). Library was constructed by Open Biosystems
(Huntsville, AL)."
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Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bogch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. Curr., Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BU425320 688 bp mRNA linear EST 29-NOV-2002
603961089F1 CSEQRBN09 Gallus gallus cDNA clone ChEST936a24 5', mRNA
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Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
   Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAMI.gov
High quality sequence stop: 626.
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0
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Best Local Similarity 66.3%; Pred. No. 0.34;
Matches 65; Conservative 0; Mismatches 33; Indels C
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/mol_type="mRNA"
/strain="Layer and broiler"
/db_xref="taxon:901"
/clone="ChEST936a24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                š
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Location/Qualifiers
                                                                                                                                                                                                         /organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
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Tel: 01612008930
Fax: 01612360409
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BU425320.1 GI:25917996
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UI-M-HB0-cow-f-04-0-UI.rl NIH BMAP_HB0 Mus musculus cDNA clone
IMAGE:30648603 5', mRNA sequence.
CN459880
CR459880.1 GI:46465606
                                                                                                                                                                                                                                                                     EST 25-JAN-2001 mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archoauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
I (bases I to 797)
Abdrakhmanov, I. 790
Plachy, J., Korn, B. and Buerstedde, J. M.
Alarge database of chicken bursal ESTs as a resource for the analysis of vertebrate gene function
Gallos, 2062-2069 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 CAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGGTACCCGGCCCAG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 CCTCAGCCRCCGGCCATTGGGGGGGGGGAGCCCCGTGGTGAGCGAGTGACAGAGTGGAGTGGAGCC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73
   146 TGCGAACCGGGACGCCACTCCGGAAGCCTTNNCCACCCGGNNCTGGCTCGGGGATTTGGC 87
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Gellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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AJ394075 dkfz426 Gallus gallus cDNA clone 17pllr1,
AJ394075
                                                           155 GCGGGGAGCCCCGTGGTGAGCGAGTGACAGAGTGGAGCCCAGAG 198
                                                                                                                      43
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                                                                                                                   86 rcredeaccccrredeacargeacagacannnnnnchnand
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/cell_type="bursal lymphocyte"
/dev_stage="2"3 weeks old"
/clone_lib="dkfz426"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 15.4%; Score 39.8; DB 1; Similarity 49.5%; Pred. No. 8.9; 98; Conservative 1; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .797
/organism="Gallus gallus"
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/clone="17p11r1"
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/strain="CB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 CAGAGGAGACACGCAGCC 211
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Best Local Similarity
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AJ394075/c
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Mammalia, Eutheria, Laurasiatheria, Carnivora, Flssipedia, Canidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ï
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 IGCCAACGTGGAATTCACTCAGGTACCCGGCCCAGCC----TCAGCCRCCGGCCATTGGG 154
                                                                                                                                                                                                          /note="Vector: pOTB7; Site 1: EcoR1; Site 2: XhoI; oligo dt priming from poly A+ RNA, directionall\overline{y} cloned"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCTCAGCTCATCCGCTATGCTGGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCC 98
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/lab host="EMDH10B"
/clone_lib="GLGC-LIB0001-cf Canis familiaris Normalized
Mixed Tissue cDNA Library"
/note="Organ: heart, liver, kidney, testis, and brain;
Vector: pCMVSport6.0; Site_1: Not1; Site_2: Sal1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 TGGAATGCTCAGCTCATCCGCTATGCTGCTACCAGATGCCAGATGGCAGCATCAGAGGG
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                      /dev_stage="0-18h embryos"
/clone_lib="Drosophila pseudoobscura embryonic cDNA
library"
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                                                                                                                                                                                                                                                                                                                                16.4%; Score 42.4; DB 8; Length 1171; 52.9%; Pred. No. 1.9; tive 0; Mismatches 81; Indels 0;
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Pred. No. 6.6;
0; Mismatches 71; Indels 4
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organism="Drosophila pseudoobscura"
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Tel: 301 987 1700
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                            /mol_type="mRNA"
/db_xref="taxon:7237"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: qliu@genelogic.com.
Location/Qualifiers
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/strain="beagle"
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Canis familiaris
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1 Similarity 54.3%;
89; Conservative 0
                                                        /db_xref="ta
/clone="K7"
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Gene Logic Inc.
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Beloniformes; Adrianichthyidae; Oryzias.
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/dev stage="whole eye"
/dev stage="whole eye"
/dev stage="mbryo 12.5,13.5,14.5 dpc"
/dev stage="mbryo 12.5,13.5,14.5 dpc"
/dev stage="bhlow (TI phage resistant)"
/clone lib="NIH BMAP HBO"
/note="Organ: Eye; Vector: pXX- Asc; Site 1: EcoR I;
Site 2: Not I: The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarcse
gel.First strand cDNA was size fractionated on a 1% agarcse
gel.First strand cDNA was synthesis was primed with Oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction ,ligated
with EcoR I adaptor , digested with NotI and then cloned
directionally into pXX-Asc vector . The library tag
sequence located between the Not I site and the polyA tail
is TAATTGAAGT. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BJ733387 MF015DA CDNA Oryzias latipes CDNA clone MF015DA022j07 5',
                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.

Email: cgapbs.r@mail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa

Tissue Procurement: Dr. James Lin University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/mousefl.html

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
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                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Musinae; Lo 771)
                                                                                                                                                        MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/organism="Mus musculus"
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/clone="IMAGE:30648603"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: pXX-5.
Location/Qualifiers
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/strain="C57BL/6"
        Mus musculus (house mouse)
Mus musculus
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BJ733387
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
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Matches
                                                                                                                                     REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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1 (bases 1 to 721)
Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
Medaka EST Project in Takeda's lab
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                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
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/db_xref="taxon:8090"
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/sex="mixture of female and male"
/fissue_type="whole embryo"
/dev_stage="organogenesis stage 35"
/clone_lib="MF015DA cDNA"
                                                    Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6856
                                                                                                                                                                                                                                                                    /organism="Oryzias latipes"
                                                                                                                                                                                                         102 CAACGTGGAATTCACTCAGGT 122
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Best Local Similarity 67.99
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December 13, 2005, 16:17:25 ; Search time 142 Seconds (without alignments) 3229.654 Million cell updates/sec
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1 cagcggagtgatggcaagca......ttgttccccagctgtgcatc 258
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1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*

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9: /cgn2_6/ptodata/1/ina/RP_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RP_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                1303057 segs, 888780828 residues
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 11841, A Sequence 15484, A Sequence 1342, App Sequence 11, Appl Sequence 1, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 11, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 20, Appli
SUMMARIES	US-09-949-016-11841 US-09-949-016-15484 US-09-949-016-1342 US-09-949-016-3342 US-09-949-016-3342 US-09-126-109-11 US-09-126-109-11 US-08-144-178 US-08-265-046-1 US-08-265-046-1 US-08-265-046-1 US-08-265-046-1 US-08-265-046-1 US-08-265-046-1 US-09-123-708-1
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20,	1363	Sequence 25, Appl Sequence 25, Appl Sequence 1, Appli Sequence 17, Appl Sequence 17, Appl	Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 11, Appl
US-09-123-624-3 US-08-880-342-20 US-09-068-506-1	US-09-0168-508-01 US-09-016-434-1234 US-08-616-434-1369 US-08-896-053-5 US-09-123-708-5 US-09-123-624-5	US-08-809-917-25 US-09-419-371-25 US-07-908-245-1 US-08-258-261B-17 US-08-456-837-17	US-08-457-8-68-17 US-08-458-076A-17 US-08-457-335A-17 US-08-729-214-17 US-09-028-934-17 US-08-761-258-11
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ALIGNMENTS

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Craig et al. Craig et al. OLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF MATH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TOWARDER: US/09/949,016 2000-04-14 ABER: 60/231,768 000-10-20 GBER: 60/231,498 1 207012 C Windows Version 4.0	3; Length 47419; 0; Indels 0;	1 CAGCGGAGTGATGGCAAGGACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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RESULT 1 US-09-949-016-11841, ADD 18 Sequence 11841, ADD 18 SEGUENCE OF INVENTION TITLE OF INVENTION FILE REFERENCE: CURRENT FILING DATE PRIOR PELING DATE PRIOR APPLICATION PRIOR APPLICATION PRIOR FILING DATE PRIOR FILING	Query Match Best Local Matches 25	
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JUNEAR PAPELICATION NUMBER: 60/231,796

PRICE APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

PRIOR PILING DATE: 2000-09-08
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Pred. No. 5.6e-24;
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Pred. No. 5.6e-24;
0; Mismatches 1;
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Patent No. 6771856
GAPBERAL INFORMATION:
APPLICANT: Thigpen, Anice
APPLICANT: Hohmeier, Hans-Ewald
APPLICANT: Newgard, Christopher B.
APPLICANT: Newgard, Christopher B.
APPLICANT: Unger, Roger H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.78;
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Best Local Similarity 99.2
Matches 121; Conservative
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Matches 121; Conservative
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                              ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3742
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ORGANISM: Human
        LENGTH: 3853
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                                                                                                                      Sequence 15484, Application US/09949016

Sequence 15484, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/291,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PLILNG DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTESEQ for Windows Version 4.0

SEQ ID NO 15484
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; Patent No. 6812339
; GENERAL INCOMMATION:
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21492 ACAGAGTGGAGCCCAGAGGAGACACGCAGGCTTACAGACTCACAGAGGCCCGTCTT 21551
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99.8%; Score 257.6; DB 3; Length 47420;
Best Local Similarity 99.6%; Pred. No. 7e-62;
Matches 257; Conservative 1; Mismatches 0; Indels 0;
21552 GTTCCCCAGCTGTGCATC 21569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 GTTCCCCAGCTGTGCATC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: Human
US-09-949-016-15484
                                                                                                        -09-949-016-15484
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61 GGCTACCAGATGCCAGATGGCAGCATCAAAGGGACCCTGCCAACGTGGAATTCACTCAG 120
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; Sequence 1, Application US/08314917
; Patent No. 5468630
; GENERAL INFORMATION:
    APPLICANT: Billiar, Timothy R.
    APPLICANT: Geller, Andreas K.
    APPLICANT: Geller, David A.
    TITLE OF INVENTION: CDNA Clone for Human Inducible Nitric
    TITLE OF INVENTION: Oxide Synthase And Process for Preparing Same
    NUMBER OF SEQUENCES: 2
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Arnold B. Silverman
    ADDRESSEE: Arnold B. Silverman
    ADDRESSEE: Arnold B. Silverman
    STREET: 600 Grant Street, 42nd Floor
    CITY: Pittsburgh
    STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGTATGCT
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Pred. No. 5.7e-24;
0; Mismatches 1; Indels 0;
            ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-00:
TELECOMMUNICATION INFORMATION:
TELEFAX: (550) 845-4166
INFORMATION FOR SEQ ID NO: 1478:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.2%;
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 4062 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
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US-09-016-434-1478
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Sequence 1478, Application US/09016434

Parent No. 6500938

GENERAL INFORMATION:

APPLICANT: Janice Au-Young

APPLICANT: Jeffrey J. Sellhamer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

TITLE OF INVENTION: PATHWAY GENE EXPRESSION

TITLE OF SEQUENCES: 1490
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46.7%; Score 120.4; DB 3; Length 4062;
Best Local Similarity 99.2%; Pred. No. 5.7e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0;
APPLICANT: Shimabukuro, Michio
APPLICANT: Chen, Guaxun
APPLICANT: Rhodes, Christopher J.
APPLICANT: Rhodes, Christopher J.
APPLICANT: Cousin, Sigrum R.
APPLICANT: Cousin, Sharon
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
TITLE OF INVENTION: TO NO-MEDIATED CYTOTOXICITY
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                         STREET: P.O. box 112.2
CITATE: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,109
FILING DATE: 30-JUL-1998
CLASSIFICATION ON TAR
APPLICATION NUMBER: US 60/055,092
FILING DATE: 30-JUL-1997
FILING DATE: 30-JUL-1997
FILING DATE: 03-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: MCMIllian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: UTSD:560
TELEPHONE: (512) 414-7577
INFORMATION POR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 4062 base pairs
WUDE: LINGTHERMACTERISTICS:
LENGTH: A062 base pairs
                                                                                                                                                                                                                               Arnold, White & Durkee
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
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                                                                                                                                                                                                                               ADDRESSEE:
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1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAĞCTCATCCGCTATGCT
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APPLICANT: David A. Geller
APPLICANT: Richard L. Simmons
TITLE OF INVENTION: Inducible Nitric Oxide Synthase
TITLE OF INVENTION: Gene for Treatment of Disease
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lewis F. Gould, Jr.
ADDRESSEE: Lewis F. Gould, Jr.
STREET: 1700 Market Street, Suite 3232
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA
DESCRIPTION: Human Hepatocyte Inducible Nitric Oxide
DESCRIPTION: Synthase CDNA Clone
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                          COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: STATEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIT Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,046
FILING DATE: 24-JUN-1994
CLASSIFICATION: 536
ATTONNEY/AGENT INFORMATION:
NAME: GOLId, Lewis F. Jr.
REGISTRATION NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 119130
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10 PORMATION:
TELEFRAX: (215) 575-6015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 46.7%; Score 120.4; DB 2; Best Local Similarity 99.2%; Pred. No. 5.7e-24; Matches 121; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Induced Human Hepatocyte RNA
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LOCATION: 207..3668
IDENTIFICATION METHOD: Experiment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
LIBRARY: Lambda Zap II CDNA
CLONE: pHINOS
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SEQUENCE CHARACTERISTICS:
LENGTH: 4145 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNITS: unknown
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ORIGINAL SOURCE:
TISSUE TYPE: 1
                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                               19103
                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA
DESCRIPTION: Human Hepatocyte Inducible Nitric Oxide
DESCRIPTION: Synthage cDNA Clone
HYPOTHETICAL: NO
             ZIP: 15219
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/314,917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Induced Human Hepatocyte RNA
                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/981,344
FILING DATE: 25-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Arnold B.
REGISTRATION NUMBER: 2,614
REFERENCE/DOCKET NUMBER: 116972
TELECOMMUNICATION INFORMATION:
TELEPHONE: (412) 566-6000
TELEPHONE: (412) 566-6099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 207..3668
IDENTIFICATION METHOD: Experiment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08265046; Patent No. 5658565; GENERAL INFORMATION:
APPLICANT: Timothy R. Billiar
APPLICANT: Rdith Tzeng; APPLICANT: Andreas K. Nussler
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 866172
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4145 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLONE: PHINOS
POSITION IN GENOME:
CHROMOSOWE/SEGMENT: unknown
MAP POSITION: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
LIBRARY: Lambda Zap II CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNITS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1071 CT 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
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                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-314-917-1
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1011 GGCTACCAGATGCCAGATGGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 1070
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                                                                                                                                                                                                                                                                                       Sequence 1, Application PCTUS9311401
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Nussiler, Andreas K.
APPLICANT: Glamons, Richard L.
TITLE OF INVENTION: CDNA Clone for Human Inducible Nitric
TITLE OF INVENTION: Oxide Synthase And Process for Preparing Same
TITLE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER FALABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: TEM PC compatible

COMPUTER: TEM PC compatible

COMPUTER: TEM PC compatible

COMPUTER: TEM PC compatible

COMPUTER: PatentIn Release #1.0, Version #1.25

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURSTRICATION NUMBER: PT/US93/11401

ATONEY/AGENT INFORMATION:

REGISTRATION NUMBER: US/07/981,344

CLASSIFICATION NUMBER: 116972

REGISTRATION NUMBER: 116972

TELEFRONCE/DOCKET NUMBER: 116972

TELEFRAMICH/ON INFORMATION:

TELEFRAMICH/ON SEQ ID NO: 1:

TELEFRAMICH/ON FOR SEQ ID NO: 1:

MANG: SEQUENCE CHARACTERISTICS:

LINFORMATION FOR SEQ ID NO: 1:

LENGTH: 4145 base pairs

TYPE: MORGANISTICS:

LENGTH: A145 base pairs

TYPE: MORGANISTICS:

TYPE: MORGA
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99.2%; Pred. No. 5.7e-24;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Arnold B. Silverman
ADDRESSEE: Eckert Seamans Cherin & Mellott
STREET: 600 Grant Street, 42nd Floor
CITY: Pittsburgh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Induced Human Hepatocyte RNA
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LOCATION: 207..3668
IDENTIFICATION METHOD: Experiment
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CHROMOSOME/SEGMENT: unknown
MAP POSITION: unknown
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LIBRARY: Lambda Zap II CDNA
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Best Local Similarity 99.2
Matches 121; Conservative
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ORIGINAL SOURCE:
TISSUE TYPE: IN
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                                                                     121 GT 122
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                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Billiar, Timothy R.
APPLICANT: Billiar, Andreas K.
APPLICANT: Bulliar, Andreas K.
APPLICANT: Geller, Andreas K.
APPLICANT: Gimmons, Richard L.
TITLE OF INVENTION: CDNA Clone for Human Inducible Nitric
TITLE OF INVENTION: Oxide Synthase And Process for Preparing Same
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lewis F. Gould, Jr.
ADDRESSEE: Lewert Seamans Cherin & Mellott
STREET: 1700 Market St. Suite 3232
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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46.7%; Score 120.4; DB 2; Length 4145;
Best Local Similarity 99.2%; Pred. No. 5.7e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: CDNA
DESCRIPTION: Human Hepatocyte Inducible Nitric Oxide
DESCRIPTION: Synthase CDNA Clone
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,522
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GOLIG, US., Lewis F.
REGISTRATION NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 116972-6
TELEPRAY: (215) 575-6020
TELEPRAX: (215) 575-6015
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LOCATION: 207..3668
IDENTIFICATION METHOD: Experiment
                                                                         Sequence 1, Application US/08465522
Patent No. 5882908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHROMOSOME/SEGMENT: unknown MAP POSITION: unknown
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LIBRARY: Lambda Zap II CDNA
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4145 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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UNITS: unknown
FEATURE:
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ORIGINAL SOURCE:
TISSUE TYPE: 1
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951 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010
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Patent No. 6607879
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
TOWNESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3144 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CAGCGGAGTGATGGCAAGACTTCCGGGTGTGAATGCTCAGCTCATCCGCTATGCT
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       Length 4145;
                                                Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
SUGRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 46.7%; Score 120.4; DB 3; Best Local Similarity 99.2%; Pred. No. 5.7e-24; Matches 121; Conservative 0; Mismatches 1;
Score 120.4; DB 6;
Pred. No. 5.7e-24;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
CLASSIFICATION:
APPLICATION:
CLASSIFICATION:
ATTORNEY, AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 1407:
SEQUENCE CHARACTERISTICS:
LENGTH: 4164 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  Query Match
Best Local Similarity 99.2%;
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: CALIFORNIA COUNTRY: USA
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US-09-023-655-1407
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US-09-023-655-1407
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                             951 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCCAGCTCATCCGCTATGCT 1010
                                                                                                                       1011 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 1070
                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: University of Pittsburgh of the Commonwealth System of Higher
APPLICANT: University of Pittsburgh of the Commonwealth System of Higher
TITLE OF INVENTION: Inducible Nitric Oxide Synthase
TITLE OF INVENTION: Gene for Treatment of Disease
TITLE OF INVENTION: Gene for Treatment of Disease
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lewis F. Gould, Jr.
ADDRESSEE: Lewis F. Gould, Jr.
STREET: 1700 Market Street, Suite 3232
CITY: Philadelphia
                                                                                               61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4145 base pairs
TENGTH: 0416 base pairs
TYPE: nucleic acid
STRANDEDNES: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
DESCRIPTION: Human Hepatocyte Inducible Nitric Oxide
DESCRIPTION: Synthase CDNA Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENDE: AND COURCE!
TISSUE TYPE: Induced Human Hepatocyte RNA IMMEDIATE SOURCE:
LIBRARY: Lambda Zap II CDNA CLONE: PHINOS
POSITION IN GENOME:
CHROMOSOME/SEGMENT: UNKNOWN
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NAME/KEY: CDS
LOCATION: 207..3668
| IDBNIFTCATION METHOD: Experiment
PCT-US95-07849-1
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ATTORNEY/AGENT INPORMATION:
NAME: GOULd, Lewis F. Jr.
REGISTRATION NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 11913
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 575-6015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAP POSITION: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                          RESULT 11
PCT-US95-07849-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                        Sequence 1, Application US/09123708

Sequence 1, Application US/09123708

GENERAL INFORMATION:

APPLICAMT: SCHRADER,

TITLE OF INVENTION: TREAPMENT OF VASCULAR DISORDERS

TITLE OF INVENTION: TREAPMENT OF VASCULAR DISORDERS

TITLE OF INVENTION: UNMERR: US/09/123,708

CURRENT APPLICATION NUMBER: US/09/123,708

CURRENT FILING DATE: 1998-07-28

EARLIER APPLICATION NUMBER: P4411402.8

EARLIER FILING DATE: 1994-03-31

SARLIER PILING DATE: 1994-03-31

SARLIER PILING DATE: 1994-03-31

SEQIEMARE: PALENTIN VOS: 6

SOFTWARE: PALENTIN VOS: 6

SEQIEMARE: PALENTIN VOS: 6

SEQUENTIAL OF TREAPMENT O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CAGCGGAGTGATGCCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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Best Local Similarity 84.4%; Pred. No. 5.8e-16;
Matches 103; Conservative 0; Mismatches 19; Indels
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Pred. No. 5.8e-16;
0; Mismatches 19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 35.5
Best Local Similarity 84.4
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1038 TT 1039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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970 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1029
                                                           61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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APPLICANT: Xie, Qiao-wen

APPLICANT: Nathan, Carl F.

APPLICANT: Mumford, Richard A.

APPLICANT: Calaycay, Jimmy Ramos

TITLE OF INVENTION: DNA Encoding Inducible Nitric Oxide Synthase

TITLE OF SQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSE: Merck & Co., Inc.

STRET: 126 East Lincoln Avenue

CITY: Rahway

STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,
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Pred. No. 5.7e-16;
0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh Centris650
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,812
FILING DATE: No. 5766909 Available
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/841,641
FILING DATE: 02-FEB-1992
ATTORNEY/AGRAY INFORMATION:
NAME: Wallen, John W III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 186581A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08147812
Patent No. 5766909
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Best Local Similarity 84.4%;
Matches 103; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4041 bases
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STRANDEDNESS: sing]
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TELEX: 1:
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US-08-147-812-4
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us-10-713-137-1.rni

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1477;
SEQUENCE CHARACTERISTICS;
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TYPE: nucleic acid
STRANDEDNESS: single
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US-09-016-434-1477
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LIBRARY: GENB
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                             978 GGCTACCAGATGCCCGATGGCACCATCAGAGGGATGCTGCCACCTTGGAGTTCACAG 1037
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61 GGCTACCAGATGCCAGATGGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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                                                                                                                                                                                                                                                      Sequence 6, Application US/08147812
Patent No. 5766909
GENERAL INFORMATION:
APPLICANT: Asia, Oiao-wen
APPLICANT: Nathan, Carl F.
APPLICANT: Nathan, Carl F.
APPLICANT: Olao-wen
APPLICANT: Olaycay, Jimmy Ramos
TITLE OF INVENTION: DNA Encoding Inducible Nitric Oxide Synthase
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 East Lincoln Avenue
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Pred. No. 5.8e-16;
0; Mismatches 19; Indels 0;
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MEDIUM TYPE: Floppy Disk
COMPUTER: Macincoh Centrise50
OPERATING SYSTEM: Macincoh Centrise50
OPERATING SYSTEM: Macincoh 7.0.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,812
FILING DATE: No. 5766909 Available
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/841,641
APPLICATION NUMBER: 07/841,641
ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 186581A
TELECOMMUNICATION INFORMATION:
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Best Local Similarity 84.4%;
Matches 103; Conservative (
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(908) 594-4720
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TELEX: 138825
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 4165 bases
TYPE: nucleic acid
US-08-147-812-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Jersey
: USA
                                                                                                                                       1038 TT 1039
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STATE: New
COUNTRY: US
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US-08-147-812-6
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US-09-016-434-1477

US-09-016-434-1477

Sequence 1477, Application US/09016434

Sequence 1477, Application US/09016434

Patent No. 650038

APPLICANT: Janice Au-Young

APPLICANT: Janice Au-Young

APPLICANT: Janice Au-Young

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

TITLE OF INVENTION: PATHWAY GENE EXPRESSION

NUMBER OP SEQUENCES: 1490

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Patent No. 5834306
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Namette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFTCATION:
PARON APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 30.3%; Score 78.2; DB 3; 18est Local Similarity 77.2%; Pred. No. 3e-12; Matches 95; Conservative 0; Mismatches 28;
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ADDRESSEE: Dehlinger & Associates
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INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
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                                               STREET: 350 CC...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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30.3%; Score 78.2; DB 2; Length 4353;
Best Local Similarity 77.2%; Pred. No. 3.1e-12;
Matches 95; Conservative 0; Mismatches 28; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human NOS-1 gene, Fujisawa, et al,
INDIVIDUAL ISOLATE: J. Neurochem 63:140 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Thrapeutic Constructs
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:

NAME: Sholtz, Charles K.

REFERENCE/DOCKET NUMBER: 8255-0018
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELERPORE: (415) 324-0980
TELERPORE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERICATION:

SEQUENCE CHARACTE
                             AUNESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
COUNTRY: CA
777
                       Therapeutic Constructs
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
BEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6218179
GENERAL INFORMATION:
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MOLECULE TYPE: CDNA tO MRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 4353 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
     NUMBER OF INVENTION: Th
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
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LOCATION: 1..4305
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1465 GGCTACAAGAGGCCTGACGCTCCACCCTGGGGAACCCAGCCAATGTGCAGTTCACAGAG 1524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 30.3%; Score 78.2; DB 3; Length 43
Best Local Similarity 77.2%; Pred. No. 3.1e-12;
Matches 95; Conservative 0; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human NOS-1 gene, Fujisawa, et al,
J. Neurochem 63:140 1994
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US-08-365-46A-12
Sequence 12, Application US/08365486A
Sequence 12, Application US/08365486A
Sequence 12, Application US/08365486A
APPLICANT: Webster, Keith A.
APPLICANT: Webster, Nanette H.
APPLICANT: Bishopric, Nanette H.
TITLE OF INVENTION: Therapeutic Constructs
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                 CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/880,342

FILING DATE: 23-JUN-1997

CLASSIFICATION: 514

PRIOR APPLICATION S14

PRIOR APPLICATION NUMBER: PT/1B95/00996

FILING APPLICATION NUMBER: 08/365,486

FILING APPLICATION NUMBER: 08/365,486

FILING APPLICATION NUMBER: 23-DEC-1994

ATTOMNEY/AGENT INFORMATION:

ATTOMNEY/AGENT INFORMATION:
350 Cambridge Avenue, Suite 250
                                                                   COUNTR:
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
~WEDIUM: IBM PC compatible
~WETEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615-
RELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 4353 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
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1738 cagadgacrgacggcaaacargacrrccgagrgrggaacrcgcagcrcarccgcracgcg 1797
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| Sequence 1, Application US/07642002 |
| Sequence 1, Application US/07642002 |
| Sequence 1, Application US/07642002 |
| Patchi No. 5268465 |
| GENERAL INFORMATION: APPLICANT: Bredt, David S. |
| APPLICANT: Reed, Randall |
| APPLICANT: Reed, Randall |
| APPLICANT: Snyder, Solomon H. |
| TITLE OF INVENTION: Purification and Molecular Cloning of Nitric |
| TITLE OF INVENTION: Oxide Synthase |
| NUMBER OF SEQUENCES: 2 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSE: Banner, Birch, McKie & Beckett |
| STREET: One Thomas Circle, NW |
| CITY: Washington |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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                                                                                                                                              CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIPICATION 1514
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/66
FILING DATE: 13-NOV-1995
PRIOR APPLICATION NUMBER: US/08/365,486
FILING DATE: 13-NOV-1995
PRIOR APPLICATION NUMBER: US/08/365,486
FILING DATE: 23-DEC-1994
ATFORNEY/AGENT INPORMATION:
NAME: Sholtz, Charles K.

REGISTRATION NUMBER: 38,615
REGISTRATION NUMBER: 38,615
REGISTRATION NUMBER: 38,615
REGISTRATION NUMBER: 38,615
REGISTRATION STORMATION:
TELEPHONE: (415) 324-0980
TELEFMIX: (415) 324-0980
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LEMGTH: 5057 base pairs
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                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 76.2%;
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-880-342-12
; Sequence 12, Application US/08880342
; Sequence 12, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
    APPLICANT: Webster, Keith A.
    APPLICANT: Bishopric, Nanette H.
    APPLICANT: Laderoute, Keith R.
    APPLICANT: Laderoute, Keith R.
    APPLICANT: Laderoute, Keith R.
    APPLICANT: Laderoute, Reith R.
    APPLICANT: Application Tissue Specific Hypoxia Regulated
    TITLE OF INVENTION: Thesapeutic Constructs
    NUMBER OF SEQUENCES: 37
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Deblinger & Associates
    STREET: 350 Cambridge Avenue, Suite 250
                                                                                                         COUNTRY: USA

ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFTCATION: 110FORMATION:
NAME: Sholtz, Charles K:
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 9255-0018
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 5057 base pairs
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDIVIDUAL ISOLATE: rat bNOS cDNA
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MOLECULE TYPE: CDNA tO MRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 29.3
Best Local Similarity 76.2
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 349..4638
                  STREET: 350
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29.1%; Score 75; DB 2; Length 4780
Best Local Similarity 75.6%; Pred. No. 2.4e-11;
Matches 93; Conservative 0; Mismatches 30; Indels
                                                         CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
FILING DATE: 23-DEC-1994
FILING DATE: 13-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAMME: Sholtz, Charles K.

REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018
TELECHONE: (415) 324-0880
TELECHONE: (415) 324-0880
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERICS:

LENGTH: 4780 base pairs
TYPE: nucleic acid
STRANDEDNES: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human NOS-SN gene, Nakane,
FEBS Lett 316:175 (1993)
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CURRENT FILING DATE: 1998-07-28
EARLIER APPLICATION NUMBER: 08/553,503
EARLIER PILING DATE: 1996-03-01
EARLIER FILING DATE: 1996-03-01
EARLIER FILING DATE: 1994-03-31
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 4780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Cytomegalovirus
US-09-123-708-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 431..4732
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ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,002
FILING DATE: 19910118
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: Kagan, Sarzah A.
NAMME: Kagan, Sarzah A.
REGISTRATION NUMBER: 1107.033576
TELEPANE: (202) 296-5500
TELEPANE: (202) 296-5500
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5108 base pairs
TYPE: NUCLEIC ACID
STRANDEDINESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
ORGANISM: Rattus rattus
TISSUE TYPE: Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 29.37
Best Local Similarity 76.29
Matches 93; Conservative
                                                                                         ZIP: 20005
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 400..4686
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
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STATE:
COUNTRY: USA
20005
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ANTI-SENSE: N
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      Palo Alto
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HYPOTHETICAL: NO
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                                                               94306
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US-08-880-342-20
                                               COUNTRY:
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                                                                                     1892 GGCTACAAGCACCGTGACGGCTCCACCCTGGGGACCCAGCCAATGTGCAGTTCACAGAG 1951
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SCHRADER, Jurgen
APPLICANT: GOBECKE, Axel
TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC
TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
FILE REFERENCE: 511169-2004
CURRENT APPLICATION NUMBER: US/09/123, 624
CURRENT FILING DATE: 1998-07-28
PRIOR FILING DATE: 1996-03-01
PRIOR FILING DATE: 1996-03-01
PRIOR FILING DATE: 1994-03-31
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PARCELIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1832 cagaddacadacddaadacacaactrccaarcragaacrcccagcrcarccgcracgcr 1891
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                                                                                                                                               61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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                                                             1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                       Gaps
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APPLICANT: Webster, Keith A.
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Macroute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRIGGE & Associates
STREET: 350 Cambridge Avenue, Suite 250
75.6%; Pred. No. 2.4e-11;
tive 0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30; Indels
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75.6%; Pred. No. 2.4e-11;
tive 0; Mismatches 30;
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Patent No. 6218179
                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09123624
Patent No. 6149936
GENERAL INFORMATION:
Best Local Similarity 75.6
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 29.1
Best Local Similarity 75.6
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                          1952 ATA 1954
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1832 CAGAGGACAGACGCCAAGCACGACTTCCGAGTCTGGAACTCCCAGCTCATCCGCTACGCT 1891
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Batent No. 6569618
GENERAL INFORMATION:
APPLICANT: YASUE, Hirofumi
APPLICANT: YOSHIMURA, Kumamoto
TITLE OF INVENTION: DIAGNOSIS OF DISEASES ASSOCIATED WITH CORONARY
TITLE OF INVENTION: THITCHING
FILE REFERENCE: 0032-245P
CURRENT FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 29.1%; Score 75; DB 3; Length 4780; Best Local Similarity 75.6%; Pred. No. 2.4e-11; Matches 93; Conservative 0; Mismatches 30; Indels
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               COMPUTER: PLOPPY disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
RICH APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/1B95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: SADOLE, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 32-0018.30
TELEFAX: (415) 334-0960
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 4780 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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Patent No. 6565918

GENERAL INFORMATION:
APPLICANT: YASUE, Hirofumi
APPLICANT: YOSHIMURA, Kumamoto
TITLE OF INVENTION: TWITCHING
FILLE REFERENCE: 0032-245P
CURRENT APPLICATION NUMBER: US/09/068,506A
CURRENT FILLNG DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 72
CORPORADE: PARCET OF THE SECONDATE 
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Patent No. 650038
GENERAL INFORMATION:
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
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                                                                                                                                                                                                 FEATURE:
; OTHER INFORMATION: nnnnnnnnn = Intervening sequences of introns
US-09-068-506-1
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                                                                                                                                                                                                                                                                                                                                                          21.9%; Score 56.4; DB 3; Length 9208; 66.4%; Pred. No. 4.1e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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        SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 9208
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Matches 80; Conservative
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Matches 81; Conservative
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US-09-068-506-2
                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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LENGTH: 3612
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US-09-068-506-2
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61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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US-09-016-434-1369
is Sequence 1369, Application US/09016434
j Patent No. 6500938
j Patent No. 6500938
j Patent No. 6500938
j Patent John Companion Patent Carlon of Signation in Applicant: Janice Au-Young
j Applicant: John Composition For THE DETECTION OF SIGNALING
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS: 1490
CORRESPER: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
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                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
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21.2%; Score 54.8; DB 3;
Best Local Similarity 65.6%; Pred. No. 9.5e-06;
Matches 80; Conservative 0; Mismatches 42;
PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                        FILING LALL CALLOR CLASSIFICATION:
CLASSIFICATION:
NAME: Zeller, Karen J.
REGISTRATION UNDBER: 37,071
REFRENCE/DOCKET NUMBER: PA-O'
TELECOMMUNICATION INFORMATION:
TRIRPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
INPORMATION FOR SEQ ID NO: 1234:
SEQUENCE CHARACTERISICS:
LENGTH: 3690 base pairs
TYPE: nucleic acid
  ADDRESSEE: INCYTE PHARMACE
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                  HEREWITH
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                                    PALO ALTO
CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , LIBRARY; GENBANK
; CLONE: 9189259
US-09-016-434-1234
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STRANDEDNESS:
                                                                                 USA
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                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: PALO STATE: CALI COUNTRY: US ZIP: 94304
                                                                                                   ZIP: 94304
                                                            STATE: CA
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760 CAGCGCCCCCGGGCCGCGGAACATCCGGAACAGCCAGCTGGTGCGCTACGCA 819
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APPLICANT: SCHRADER, Juergen
APPLICANT: SCHRADER, Juergen
APPLICANT: GENERAL
APPLICANT: GOBERCKE, Arel
TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC
TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
FILE REFERENCE: 511169-2003
CURRENT FPLING DATE: 1998-01-28
EARLIER APPLICATION NUMBER: 08/553,503
EARLIER PILING DATE: 1996-03-01
EARLIER FILING DATE: 1996-03-01
EARLIER FILING DATE: 1994-03-31
NUMBER OF SEQ ID NOS: 6
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                                     CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/021,912
FILING DATE: 17-JUL-1996
ATTORNEY/AGENT INPORMATION:
NAME: Millonig, Robert C.
REGISTRATION NUMBER: 34,395
REFERENCE/DOCKET NUMBER: 0609.4280001/JAG/RCM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2600
TELEPHONE: CASA INFORMATION: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4099 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
20.0%; Score 51.6; DB 3;
Best Local Similarity 62.3%; Pred. No. 7.5e-05;
Matches 81; Conservative 0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09123708
Patent No. 6146887
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ORGANISM: Cytomegalovirus
US-09-123-708-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear / MOLECULE TYPE: CDNA US-08-896-053-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GT 122
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LENGTH: 4097
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Patent No. 6720309
GENERAL INFORMATION:
APPLICANT: Unanssens, Stefans
APPLICANT: Bloch, Kenneth D.
APPLICANT: Collen, D sir
TITLE OF INVENTION: Treating Pulmonary Hypertension Using Adenoviral-Mediated
TITLE OF INVENTION: Transfer of the Nitric Oxide Synthase Gene
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                748 casciccrissicas de de contra de la contra de la contra de cont
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Berfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Berfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Berfect 6.1 for Windows/MS-DOS 6.2
GURRENT APPLICATION DATA:
PRIOR APPLICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: BILING DATE:
APPLICATION NUMBER: BILING DATE:
APPLICATION NUMBER: BA-OSSES FREENCE/DOCKET NUMBER: BA-OSSES
TELECOMMUNICATION INFORMATION:
TELECHAN: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1369:
SEQUENCE CHARACTERISTICS:
LEGGH: 4035 base pairs
TYPE: NUCLAIC acid
STREET ALOLATION INFORMATION:
TELECHAN: A035 base pairs
TYPE: NUCLAIC acid
STREET NUCLAIC acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Sterne, Kessler, Goldstein & Fox P.L.L.C. CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LIBRARY: GENBANK
; CLONE: g434699
US-09-016-434-1369
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IMMEDIATE SOURCE:
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US-08-896-053-5
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TOPOLOGY: linear ; MOLECULE TYPE: cDNA US-08-809-917-25
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SEQ ID NO 25
LENGTH: 4491
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US-09-419-371-25
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                                                                                                                      US-09-123-624-5

US-09-123-624-5

Sequence 5, Application US/09123624

Patent No. 614996

GENERAL INFORMATION:
APPLICANT: SCHRADER, Jurgen
APPLICANT: GONECKE, Axel
TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
FILE REFREENCE: 511169-2004

CURRENT APPLICATION NUMBER: US/09/123,624

CURRENT APPLICATION NUMBER: US/09/123,624

CURRENT APPLICATION NUMBER: 08/553,503

PRIOR APPLICATION NUMBER: 4411402.8

PRIOR PILING DATE: 1994-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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20.0%; Score 51.6; DB 3; Length 4097;
Best Local Similarity 62.3%; Pred. No. 7.5e-05;
Matches 81; Conservative 0; Mismatches 49; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: APPLICANT
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES
TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02173

ZIP: 02173

CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Pacentiale
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/08809917
Patent No. 6689557
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
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121 GIACCCGGCC 130
                                      вво стстесатсс ввэ
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US-09-123-624-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 4491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FERENCE IN INFORMATION:

APPLICANT: TU11y, Timothy P.
APPLICANT: TU11y, Timothy P.
TITLE OF INVENTION: Cloning and Characterizing of Genes
TITLE OF INVENTION: Cloning and Characterizing of Genes
TITLE OF INVENTION: Associated With Long-Term Memory
FILE REFERENCE: CSHL94-03A3Z
CURRENT FILING DATE: 1999-10-14
PRIOR FILING DATE: 1999-10-17
PRIOR APPLICATION NUMBER: 08/809,917
PRIOR FILING DATE: 1997-07-07
PRIOR FILING DATE: 1997-10-06
PRIOR FILING DATE: 1994-12-21
PRIOR FILING DATE: 1994-12-21
PRIOR FILING DATE: 1994-10-07
PRIOR FILING DATE: 1994-10-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44; Indels
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Pred. No. 7.6e-05;
0; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 20.0%; Score 51.6; DB 3; Best Local Similarity 63.9%; Pred. No. 7.6e-05; Matches 78; Conservative 0; Mismatches 44;
                                                                                                                                                                                                           HEGISTRATION NUMBER: 32,227
REGISTRATION NUMBER: 32,227
REPERENCE/DOCKET NUMBER: CSHL94-03A2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEPAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 4491 base pairs
APPLICATION NUMBER: PCT/US95/13198 FILING DATE: APPLICATION NUMBER: US 08/361,063 FILING DATE: 21-DEC-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/319,866 FILING DATE: 07-OCT-1994 ATTORNEY/AGENT INPORMATION: NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 25, Application US/09419371
; Patent No. 6890516
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Best Local Similarity 63.9%;
Matches 78; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: 1598..2758
OTHER INFORMATION: /gene= "phz2"
OTHER INFORMATION: /label= ORF2
OTHER INFORMATION: /note= "Open Reading Frame #2 for DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: /gene= "phz1"
OTHER INFORMATION: /label= ORF1
OTHER INFORMATION: /note= "Open Reading Frame #1 for DNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYRE: Floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.25

COMPUTER: BM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.25

COMPUTER: DatentIn Release #1.0, Version #1.25

COMPUTER: DatentIn Release #1.0, Version #1.25

SOFTWARE: PatentIn Release #1.0, Version #1.25

COMPUTER: DatentIn Release #1.0, Ver
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Schuby, Thomas
APPLICANT: Ligon, James M.
APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Ryals, John Andrew
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:

    Ciba-Geigy Corporation
    Skyline Drive

                                                                                                                                                                                                                                      US-08-258-261B-17/c
; Sequence 17, Application US/08258261B
; Patent No. 5639949
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 2764..3597
CHER INFORMATION: /gene= "phz3"
OTHER INFORMATION: /label= ORF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                      121 GTACCCGGCC 130
                                                                                                     852 CTCTGCATCC 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 230..1594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 7 SKyll.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                          RESULT 37
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                                      ò
                                                       1320 CAACGCACAGATGCCAAGCATGATTATCGCATTTGGAATAACCAATTAATATCTTATGCC 1379
                                                                                                                                                                                                ö
                                                                                                                                    61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         732 chácicecececededececedadaciricedaricidahecaeceheciedredecinecineera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       792 dectacacacacacadarcecrcrerecerdedeaceceaceareredagareacead 851
1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Harrison, David G.
APPLICANT: Alexander, R. Wayne
APPLICANT: Murphy, T.J.
APPLICANT: Murphy, T.J.
APPLICANT: Mishida, Ken'ichi
TITLE OF INVENTION: Endothelial Nitric Oxide Synthase
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
COMPUTER: Georgia
COMPUTER: D.S.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/908,245
FILING DATE: 19920702
CLASSIFICATION: A35
ATTORNEY/AGRATION: A35
ATTORNEY/AGRATION: NUMBER: EMU 111
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-07-908-245-1
; Sequence 1, Application US/07908245
Patent No. 5498539
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 4089 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Bovine
TISSUE TYPE: Aorta
CELL TYPE: Endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: CDN
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                     121 GT 122
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CTHER INFORMATION: /gene= "phz2"

OTHER INFORMATION: /label= ORF2

OTHER INFORMATION: /label= ORF2

OTHER INFORMATION: /label= ORF2

OTHER INFORMATION: /label= ORF3

LOCATION: 2764..3597

OTHER INFORMATION: /label= ORF3

OTHER INFORMATION: /label= ORF3

OTHER INFORMATION: /label= ORF3

OTHER INFORMATION: /label= ORF4

COCATION: /label= ORF4

OTHER INFORMATION: /label= ORF4
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                                                                                                                                                                                                                                                       LOCATION: 230..1594
OTHER INFORMATION: /gene= "phz1"
OTHER INFORMATION: /label= ORF1
OTHER INFORMATION: /note= "Open Reading Frame #1 for DNA sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query March 13.7%; Score 35.4; DB 2; Length 4603; Best Local Similarity 57.8%; Pred. No. 2.4; Matches 63; Conservative 0; Mismatches 46; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 GCCGACCTGATGCAGCCGCCGCATCGGAAGCCCACTCGCTGACGTCG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: 1..4603
COTHER INPORMATION: /note= "Four open reading frames
OTHER INFORMATION: Example 18 of the specification."
US-08-456-837-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ligon, James M.
APPLICANT: Bigon, James Joseph
APPLICANT: Beck, James Joseph
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synititie OF INVENTION: antipathogenic sul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 17, Application US/08457342; Patent No. 5662898
                        SEQUENCE CHARACTERISTICS:
LENGTH: 4603 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schupp, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Schupp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Hawthorne
                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 230.
                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 39
US-08-457-342-17/c
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                     FEATURE:
NAME/KEY: misc_feature
LOCATION: 3597..4262
CTHER INFORMATION: /note= "Open Reading Frame #4 of DNA sequence. This informat OTHER INFORMATION: | frepeated in SEQ ID NO:21 due to overlapping ORFs."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..4603
OTHER INFORMATION: /note= "Four open reading frames
OTHER INFORMATION: | note= "Four open reading frames
OTHER INFORMATION: Example 18 of the specification."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
   OTHER INFORMATION: /note= "Open Reading Frame #3 for DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 13.7%; Score 35.4; DB 2; Length 4603; Best Local Similarity 57.8%; Pred. No. 2.4; Matches 63; Conservative 0; Mismatches 46; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 GOCGACCTGATGCAGGCGGCGATCGGAAGCGCACTCGCTGACGTCG 61
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,837
FILING DATE: 01-JUN-1995
CLASSIFICATION NUMBER: 08/457,205
FILING APPLICATION NUMBER: 08/457,205
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/457,205
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT Schupp, Thomas
APPLICANT Ligon, James M.
APPLICANT Hill, Dwight Steven
APPLICANT Hill, Dwight Steven
APPLICANT Ryals, John Andrew
APPLICANT Ryals, John Andrew
APPLICANT Lam, Stephen Ting
APPLICANT Hammer, Phillip E.
APPLICANT Hammer, Phillip E.
APPLICANT Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Elmer, James Scottons:
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
TELECOMMUNICATION INPORMATION:
TELEPHONE: 919-541-8614
TELEFAX: 919-541-8619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Ciba-Geigy Corporation
7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDUUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17, Application US/08456837 Patent No. 5643774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 7 Skylir
CITY: Hawthorne
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Schupp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-456-837-17/c
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/gene= "phz3"
/label= ORF3
/note= "Open Reading Frame #3 for DNA sequence"
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/label= ORF1
/note= "Open Reading Frame #1 for DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene= "phz2"
/label= ORF2
/note= "Open Reading Frame #2 for DNA sequence"
  109 GGCGACCTGATGCAGGCCGGCGCATCGGAAGCGCACTCGCTGACGTCG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                              APPLICANT: Ligon, James M.
APPLICANT: Beck, James Joseph
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Lam, Stephen Ting
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Pallilip BAPPLICANT: Hammer, Pallilip BAPPLICANT: Uknes, Scott Joseph
                                                                                                  Sequence 17, Application US/08457646A Patent No. 5679560 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                 APPLICANT: Schupp, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 4603 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: CDS
LOCATION: 2764..3597
OTHER INFORMATION: /ge
OTHER INFORMATION: /no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 230..1594
OTHER INFORMATION: /1
OTHER INFORMATION: /1
OTHER INFORMATION: /1
FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1598..2758
OTHER INFORMATION: /c
OTHER INFORMATION: //
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10532
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hawthorne
                                                            RESULT 40
US-08-457-646A-17/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This informat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEZ: misc_feature
LOCATION: 3597..4262
OTHER INFORMATION: /label= ORF4
OTHER INFORMATION: /note= "Open Reading Frame #4 of DNA sequence. This
OTHER INFORMATION: is repeated in SEQ ID NO:21 due to overlapping ORF9:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 caccecaenandecrneccaeeerrcaeeerceceeercecaeeerrrreraeceeer 110
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NAME/KEY: CDS
LOCATION: 1598..2758
OTHER INFORMATION: /Jabel= "phz2"
OTHER INFORMATION: /Jabel= ORF2
OTHER INFORMATION: /note= "open Reading Frame #2 for DNA sequence"
FEATURE:
NAME/KEY: CDS
LOCATION: /gene= "phz3"
OTHER INFORMATION: /gene= "phz3"
OTHER INFORMATION: /Jabel= ORF3
OTHER INFORMATION: /note= "Open Reading Frame #3 for DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 230..1594
OTHER INFORMATION: /gene= "phz1"
OTHER INFORMATION: /label= ORF1
OTHER INFORMATION: /note= "Open Reading Frame #1 for DNA sequence"
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LOCATION: 1.4603
OTHER INFORMATION: /note= "Four open reading frames
OTHER INFORMATION:
OTHER INFORMATION: Example 18 of the specification."
                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/457,342
FILING DATE: 01-JUN-1995
CLASSIFICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Blmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
TELEPHONE: 919-541-8689
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTER ISTICS:
LENGTH: 4603 base pairs
TYPE: nucleic acid
STRANDEDNESS: stingle
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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Matches 63; Conserva
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DOCATION: 3597..4262
LOCATION: 3597..4262
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LOCATION: 3597..4262
LOCATION: 3597..4262
LOCATION: 15977..4262
LOCATION: 15 repeated in SEQ ID NO:21 due to overlapping ORFs."
FRATURE:
NAME/KEY: misc feature
LOCATION: 1..4603
CTHER INFORMATION: /note= "Four open reading frames
OTHER INFORMATION: Example 18 of the specification."
                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                        1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
                                                                                                                                                                                                                                                                               0; Gaps
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Best Local Similarity 57.8%; Pred. No. 2.4;
Matches 63; Conservative 0; Mismatches 46; Indels 0;
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US-10-713-137-1
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Sequence 5684, Ap
Sequence 19182, A
Sequence 19182, A
Sequence 51193, A
Sequence 51193, A
Sequence 51193, A
Sequence 19177, A
Sequence 1, Appli
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Sequence 185, Appl
Sequence 155, App
Sequence 621, App
Sequence 621, App
Sequence 10, Appl
Sequence 10, Appl
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Sequence 229, App
Sequence 622, App
Sequence 37, Appl
                                                                                                                                                                      (without alignments)
2680.276 Million cell updates/sec
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                                                                                                                                                December 13, 2005, 16:24:48; Search time 796 Seconds
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1: /cgn2 6/ptodata/1/pubpna/USO1 PUBCOMB.seq:*

3: /cgn2 6/ptodata/1/pubpna/USO8 PUBCOMB.seq:*

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                      GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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US-10-741-601-5684

US-10-741-601-19182

US-10-741-601-19182

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Listing first 45 summaries
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No.
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Sequence 1064, Ap Sequence 1477, Ap Sequence 1477, Ap Sequence 8, Appli Sequence 1234, Ap Sequence 1134, Ap Sequence 414, App Sequence 9, Appli Sequence 9, Appli Sequence 1460, App Sequence 1460, Appli Ap
                                     123, App
123, App
110, App
18, App
18, App
1064, Ap
1, App
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                                                                                                                        Sequence 1
Sequence 1
Sequence 9
                                                                Sequence Sequence
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US-10-929-182-33
US-09-751-708A-123
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US-10-428-817A-119
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US-10-631-467-966
US-10-631-467-1064
US-10-305-720-1477
US-10-105-720-1369
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US-11-097-143-14651
US-10-278-698-165
         20.4
20.0
18.7
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ALIGNMENTS

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WE-10-713-137-1
; Sequence 1, Application US/10713137
; Publication No. 220050106573A1
; GENERAL INFORMATION:
; APPLICANT: Pasha, Abdul Qadar Mohammad
; APPLICANT: Ansan, Aarif
; TILE OF INVENTION: A method of detection of predisposition
; TILE OF INVENTION: A nethod of detection of predisposition
; TILE OF INVENTION: A nethod of detection of predisposition
; TILE OF INVENTION: A nethod of Control of Decension
; TILE OF INVENTION: A nethod of Control of Decension
; TILE REFERENCE: 09755-0018US1
; CURRENT FILING DATE: 2003-11-13
; NUMBER OF SEQ ID NOS: 3
; SEQ ID NO 1
; SEQ ID NO 1
; LENGTH: 258
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Sequence 51219, Application US/10741600
; Sequence 51219, Application US/20050026169A1
; GENERAL INFORMATION; GENETIC FOLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION; MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION; MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION; MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF;
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT PILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SEQ ID NO 51219
; SEQ ID NO 51219
                                                         25433 GTACCCGGCCCCAGCCTCAGCCRCYGGCCATTGGGGCGGGGGGGCCCCRTGGTGAGCGGGGGGGGAGTG 25492
                                                                                                                                                    25493 ACAGAGTGGAGCCCAGAGAGAGACACGCAGCCCGGGCTTACAGACTCACAGGCCCGTCTT 25552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CAACGTGGAATTCACTCAGGTACCCGGCCCAGCCTCAGCCRCCGGCCATTGGGGGGGGGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 GCCCCGTGGTGAGCGAGTGACAGAGTGGAGCCCCAGAGGAGACACGCCAGCCCCGGGCTTACA 221
                                                                                                                                                                                                                                                                                                                                          RESULT 4

US-10-741-601-19182

US-10-741-601-19182

Sequence 19182, Application US/10741601

Publication No. US20040166519A1

GENERAL INFORMATION:

APPLICANT CARGILL, Michele et al.

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION UMBER: US/10/741,601

CURRENT APPLICATION NUMBER: US/10/741,601

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 26415

SEQ ID NO 19182

LENGTH: 201

LENGTH: 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 GACTCACAGGGCCCGTCTTGT 242
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                                                                                                                                                                                                                          241 GTTCCCCAGCTGTGCATC 258
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US-10-741-601-19182
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; ORGANISM: Homo sapiens
US-10-741-600-51219
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US-10-741-600-51219
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Publication No. US20050026169A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SEQ ID NO 17734
LENGTH: 55689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25313 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 25372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG
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US-10-741-601-5684

Sequence 5684, Application US/10741601

Sequence 5684, Application US/10741601

GENERAL INFORMATION:

TUTLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/10/741,601

CURRENT APPLICATION NUMBER: 2003-12-22

NUMBER OF SEQ ID NOS: 26415

SOFTWARE:

TOTHER OF SEQ ID NOS: 26415
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 256.8; DB 7; Length 55689;
Pred. No. 2.3e-70;
2; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.5%; Score 256.8; DB 8; Length 55689; 99.2%; Pred. No. 2.3e-70; tive 2; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25553 GTTCCCCAGCTGTGCATC 25570
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Best Local Similarity 99.2
Matches 256; Conservative
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                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
) ORGANISM: Homo sapiens
US-10-741-601-5684
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ORGANISM: Homo sapiens
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Best Local Similarity
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LENGTH: 55689
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; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 51193; LENGTH: 201
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                                                                                                                      Query Match
Best Local Similarity 99.0
Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                    TYPE: DNA
CORGANISM: Homo sapiens
US-10-741-600-51193
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LENGTH: 201
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US-10-741-600-51193

US-10-741-600-51193

BD1/cation No. US20050026169A1

GENERAL INFORMATION:

TITLE OF INVENTION: MYCHAIGE et al.

TITLE OF INVENTION: MYCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

TITLE REFREENCE: CL001499

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ACGIGGAATICACICAGGIACCCGGCCCAGCCICAGCCGCYGGCCATIGGGGCGGGAACC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCGTGGTGAGCGAGTGACAGAGTGGAGCCCAGAGAACACGCAGCCCGGGCTTACAGA 223
                                                                                                                                         CAACGTGGAATTCACTCAGGTACCCGGCCCAGCCTCAGCCRCCGGCCATTGGGGCGGGGA 161
                                                                                                                                                            GCCCCGTGGTGAGCGAGTGACAGAGTGGAGCCCAGAGGAGACACGCAGCCCGGGCTTACA 221
                                                                        42 TCAGCTCATCCGCTATGCTGGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                        1 TCAGCTCATCCGCTATGCTGGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGC 60
                                                                                                                                                                                                                                                                                                                                                                                US-10-741-601-19156

Sequence 19156, Application US/10741601

Sequence 19156, Application US/10741601

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: 201500

CURRENT APPLICATION NUMBER: US/10/741,601

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 26415

SEQ ID NO 19156

LENGTH: 201
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     77.8%; Score 200.6; DB 8; Length 201; 100.0%; Pred. No. 8.6e-53; ive 0; Mismatches 0; Indels 0
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Pred. No. 1.2e-52;
2; Mismatches 0
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Best Local Similarity 99.0
Matches 199; Conservative
                        al Similarity 100.
201; Conservative
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CORGANISM: Homo sapiens
US-10-741-601-19156
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          Query Match
Best Local S
Matches 201
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                                                                                                                                                                                                          163
                                                                                                                                                                                                                                     61 ACGTGGAATTCACTCAGGTACCCGGCCCAGCCTCAGCCGCYGGCCATTGGGGCGGGGAGC 120
                                                                                                                                                                                                                                                                                                                                                        121 CCCGTGGTGAGCGAGTGACAGAGTGGAGGGGGGGGAGACACGCAGCCCGGGCTTACAGA 180
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                                                                                                                                    104 ACGTGGAATTCACTCAGGTACCCGGCCCAGCCTCAGCCRCCGGCCATTGGGGCGGGAGC
                                                                                                                                                                                                                                                                                                             164 CCCCTGGTGAGCGAGTGACAGAGCCCCAGAGGAGACACGCAGCAGCCCGGGCTTACAGA
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                                                                                                   44 AGCTCATCCGCTATGCTGGCTACCAGATGCCAGATGGCAGCATCAGAGGGGGACCCTGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Publication No. US20040166519A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: CARGLLL, Michele et al.

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: UNMBER: US/10/741,601

CURRENT APPLICATION UNMBER: 108/10/741,601

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 26415

SOSTWARE: FRRESC for Windows Version 4.0
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77.6%; Score 200.2; DB 8; Length 201; 99.0%; Pred. No. 1.2e-52; tive 2; Mismatches 0; Indels 0
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US-10-741-600-51214
Sequence 51214, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
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                             61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                    439 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 498
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46.7%; Score 120.4; DB 7;
Best Local Similarity 99.2%; Pred. No. 1.1e-27;
Matches 121; Conservative 0; Mismatches 1;
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Publication No. US20030092039A1
GENERAL INFORMATION:
APPLICANT: Olson-Munoz, Marilyn C.
APPLICANT: Donald, Glen
TITLE OF INVENTION: Screening Nutraceuticals
TITLE REFERENCE: PORS-07289
CURRENT APPLICATION NUMBER: US/10/210,682
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 60/309,279
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
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US-10-220-282A-1
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NAME/KEY: CDS
LOCATION: (1).
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LENGTH: 3462
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| Sequence 3, Application US/10220282A
| Publication No. US20040053323A1
| GENERAL INFORMATION:
| APPLICANT: ISHII YOSHINORI
| APPLICANT: INAMI, MORITA
| APPLICANT: MORITA
| APPLICANT: MORITA
| APPLICANT: ACTABOUSOPCT
| CURRENT APPLICATION NUMBER: DCT/JP01/01865
| PRIOR FILING DATE: 2001-03-09
| PRIOR FILING DATE: 2001-03-10
| NUMBER OF SEQ ID NOS: 12
| SOFTWARE: PATCHILIN Version 3.1
APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SEQ ID NO 51214
LENGTH: 201
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                                                                                                                                                                                                                                                                                              DB 8; Length 201;
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Matches 121; Conservative
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; ORGANISM: Homo sapiens
US-10-741-600-51214
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ORGANISM: Homo Bapiens
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; OTHER INFORMATION:
US-10-220-282A-3
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Sequence 155, Application US/10631467
Suguence 155, Application US/10631467
Suguence 155, Application No. US20050208496A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive;
TITLE OF INVENTION: disease
TITLE OF INVENTION: disease
TITLE OF INVENTION: DATE: 2003-07-31
CURRENT APPLICATION NUMBER: US 2003-07-31
PRIOR APPLICATION NUMBER: US 2003-07-31
PRIOR FILING DATE: 2003-06
NUMBER OF SEQ ID NOS: 2006
SOFTWARE: Patentin version 3.1
SEQ ID NO 155
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46.7%; Score 120.4; DB 9;
Best Local Similarity 99.2%; Pred. No. 1.1e-27;
Matches 121; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                       Score 120.4; DB 9;
Pred. No. 1.1e-27;
                                                                                                                                                                                                                                                                                                                 0; Mismatches
        PRIOR APPLICATION NUMBER: JP 203-077212
PRIOR FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: JP 2002-229312
PRIOR FILING DATE: 2002-08-06
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 38
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; Sequence 228, Application US/10741601
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Best Local Similarity 99.2'
Matches 121; Conservative
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US-10-631-467-155
                                                                                                                                                                                       TYPE: DNA
COGANISM: Homo sapiens
US-10-631-467-38
CURRENT FILING DATE:
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                                                                                                                                                                      LENGTH: 4062
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Publication No. US20040010136A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressic TITLE OF INVENTION COMPOSITION for the Detection of Signaling Pathway Gene Expressic FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT APPLICATION NUMBER: 09/016,434
PRIOR FILING DATE: 1998-01-30
FRIOR FILING DATE: 1998-01-30
SOFTWARE: PERL PROGram
SEQ ID NO 1478
LENGHA 4062
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Publication No. US20050208496A1
GENERAL INFORMATION:
APPLICANT: Genox Research Inc.
TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive FILE OF INVENTION disease
FILE REFERENCE: 3462.1005-000
CURRENT APPLICATION NUMBER: US/10/631,467
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46.7%; Score 120.4; DB 6; Length 4062;
Best Local Similarity 99.2%; Pred. No. 1.1e-27;
Matches 121; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                Length 3855;
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; OTHER INFORMATION: Genbank ID No. US20040010136A1 g951320
US-10-305-720-1478
                                                                                                                                DB 5;
                                                                                                                              Query Match
46.7%; Score 120.4; DB 5
Best Local Similarity 80.3%; Pred. No. 1.1e-27;
Matches 98; Conservative 23; Mismatches 1
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                                            TYPE: RNA
ORGANISM: Homo sapiens
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US-10-305-720-1478
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US-10-631-467-38
                          LENGTH: 3855
                                                                                        US-10-210-682-1
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      SEQ ID NO 1
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TYPE: DNA
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Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
ITILE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
ITILE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
SUTUMBER OF SEQ ID NOS: 73997
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 6-12-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     999 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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                                     APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOLSOO
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT PILING DATE: 2003-12-22
SOFTWARE: FOREISE FOR WINDOWS Version 4.0
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Publication No. US20040166519A1
GENERAL INFORMATION:
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Matches 121, Conservative
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Matches 121; Conservative
                                                                                                                                                                                                                                                     , TYPE: DNA
, ORGANISM: Homo sapiens
US-10-741-601-228
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CORGANISM: Homo sapiens
US-10-741-600-621
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US-10-741-600-621
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US-10-182-049-3; Sequence 3, Application US/10182049; Publication No. US20050113322A1

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APPLICANT: 1918 Pharmaceuticals, Inc.
APPLICANT: 1918 Pharmaceuticals, Inc.
APPLICANT: 1916 Control of the Cont
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| Publication No. US20050113322A1
| Publication No. US20050113322A1
| GENERAL INFORMATION:
| APPLICANT: Isia Pharmaceuticals, Inc.
| APPLICANT: Las M. Cowers
| APPLICANT: Nicholas M. Dean
| APPLICANT: Las M. Cowers
| CURRENT PRICE RISP-0360
| CURRENT PILING DATE: 2002-07-27
| PRIOR APPLICATION NUMBER: 09/490,208
| NUMBER 09 Seq ID NOS: 182
| SEQ ID NO 10
| LENGTH: 4145
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99.2%; Pred. No. 1.1e-27;
tive 0; Mismatches 1;
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Best Local Similarity 99.2<sup>3</sup>
Matches 121, Conservative
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; LOCATION: (207)...(3668)
US-10-182-049-3
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FEATURE:
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; LOCATION: (1)...(4110)
US-10-182-049-10
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1011 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 1070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                              APPLICANT: Cocks, Benjamin G.
Susan G. Stuart
Jeffrey J. Sellhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION: Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 46.7%; Score 120.4; DB 7; Best Local Similarity 99.2%; Pred. No. 1.1e-27; Matches 121; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLONE: 9441452
; SEQUENCE DESCRIPTION: SEQ ID NO: 1407
US-10-641-643-1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                          Sequence 1407, Application US/10641643 Publication No. US20040077003A1 GENERAL INFORMATION:
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TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1407:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                               CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                      1071 CT 1072
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                                   121 GT 122
                                                                                                                         RESULT 20
US-10-641-643-1407
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GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION:

TOTHER REFERENCE:

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT FILING DATE:

NUMBER OF SEQ ID NOS: 73997

SOFTWARE: FRELSEQ for Windows Version 4.0
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Sequence 229, Application US/10741601
| Publication No. US20040166519A1
| Publication No. US20040166519A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| TITLE OF INVENTION:
| TITLE OF INVENTION:
| STENCEIS, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION:
| TITLE OF INVENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Pred. No. 1.1e-27;
0; Mismatches 1; Indels
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Best Local Similarity 99.2%;
Matches 121; Conservative
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Best Local Similarity 99.2%;
Matches 121; Conservative
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US-10-741-600-622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-10-741-601-229
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LENGTH: 4221
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RESULT

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Sequence 123, Application US/09870759
Patent No. US2002017551A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870, 759
CURRENT FILING DATE: 2002-01-14
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 123, Application US/09751708A
Publication No. US20030157113A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 751708
CURRENT APPLICATION NUMBER: US/09/751,708A
PRIOR APPLICATION NUMBER: US 60/173,371
PRIOR FILING DATE: 1999-12-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3690;
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SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) NAME/KEY: CDS
; LOCATION: (256)..(3690)
; OTHER INFORMATION:
US-09-870-759-123
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    NAMEKKY: CDS

    LOCATION: (256)..(3690)

    OTHER INFORMATION:

    US-09-751-708A-123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Mus musculus
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TT 857
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LENGTH: 3690
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LENGTH: 3690
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Fublication No. US20050064483A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Zang, Jingwu
APPLICANT: Anng, Jian
TITLE OF INVENTION: Gene Expression Profiling Technology for Treatment Evaluation of TITLE OF INVENTION: Multiple Sclerosis
FILE REFERENCE: HO-P02859U31
CURRENT APPLICATION NUMBER: US 100,929,182
CURRENT FILING DATE: 2004-08-30
PRIOR FILING DATE: 2003-08-28
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Version 3.3
SEQ ID NOS: 34
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46.0%; Score 118.8; DB 8; Length 4150;
Best Local Similarity 98.4%; Pred. No. 3.5e-27;
Matches 120; Conservative 0; Mismatches 2; Indels 0;
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                                                                             APPLICANT: Locze, Michael T
APPLICANT: Tahara, Hideaki
TITLE OF INVENTON: Methods And Reagents For Inducing Immunity
FILE REFERENCE: UPP--004
CURRENT APPLICATION NUMBER: US/10/688,845
CURRENT FILING DATE: 2003-10-15
PRIOR PILING DATE: 2002-10-15
PRIOR FILING DATE: 2002-10-15
SPIOR FILING DATE: 2002-10-15
SOFTWARE: Patentin version 3.1
SEQ ID NO 37
               Sequence 37, Application US/10688845
Publication No. US20040247578A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
US-10-688-845-37
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ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 4150
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Gaps

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US-10-182-049-18

US-10-182-049-18

Sequence 18, Application US/10182049

Sequence 18, Application No. US2005011332A1

Sequence 18, Explication No. US2005011332A1

Sequence 18, Explication No. US2005011332A1

SEQUENCE INFORMATION:

APPLICANT: Is a Pharmaceuticals, Inc.

APPLICANT: Is a Pharmaceuticals, Inc.

APPLICANT: Lax M. Cowsert

TITLE OF INVENTION: ANTISENSE MODULATION OF INDUCIBLE NITRIC OXIDE SYNTHASE EXPRESSIC

FILE REFERENCE: RTSP-0360

CURRENT PILING DATE: 2002-07-27

PRIOR PPLICATION NUMBER: US/10/182,049

CURRENT PILING DATE: 2000-01-24

NUMBER OF SEQ ID NOS: 182

SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    982 CAGCGGAGTGACGGCAAACATGACTTCAGGCTCTGGGAATTCACAGGTCATCCGGTACGCT 1041
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84.4%; Pred. No. 1.1e-18;
                                                                                                                                                                                                                                                                                                                              Query Match 35.5%; Score 91.6; DB 9; Best Local Similarity 84.4%; Pred. No. 1.1e-18; Matches 103; Conservative 0; Mismatches 19;
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                PRIOR APPLICATION NUMBER: 09/650,884
PRIOR FILING DATE: 2000-08-30
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.1
SEQ ID NO 100
LENGTH: 3690
  2004-09-08
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Best Local Similarity 84.4
Matches 103; Conservative
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; NAME/KEY: CDS
; LOCATION: (256)...(3690)
US-10-182-049-18
                                                                                                                                                                                                 FEATURE:
NAMEKKY: CDS
LOCATION: (256)..(3690)
CTHER INFORMATION:
US-10-937-758A-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                        TYPE: DNA ORGANISM: Mus musculus
    CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TT 1103
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Sequence 119, Application US/10428817A

Publication No. US20040214783A1

GENERAL INFORMATION:

APPLICANT: TERMAN, DAVIG S

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

FILE REPERENCE: 38373-189118

CURRENT APPLICATION NUMBER: US/10/428,918

PRIOR APPLICATION NUMBER: US 60/378,988

PRIOR PILING DATE: 2002-05-08

PRIOR PLILNG DATE: 2002-06-15

PRIOR PLILNG DATE: 2002-06-15

PRIOR PLILNG DATE: 2002-06-18

PRIOR PLILNG DATE: 2002-08-28

PRIOR PLILNG DATE: 2002-08-28

PRIOR PLILNG DATE: 2002-00-0

PRIOR PLILNG DATE: 2002-10-01

PRIOR PLILNG DATE: 2002-10-01

PRIOR PLILNG DATE: 2003-01-09

NUMBER OF SEQ ID NOS: 224

SEQ ID NO 119

LENGTH: 3690

"WOULD IN NO 119

LENGTH: 3690
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Sequence 100, Application US/10937758A
Publication No. US20050112141A1 ,
Publication No. US20050112141A1 ,
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
FITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE FILE REFERENCE: FILE REFERENCE 550884
CURRENT APPLICATION NUMBER: US/10/937,758A
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CAGCGGAGTGACGCGAAACATGACTTCAGGCTCTGGAATTCACAGCTCATCCGGTACGCT 1041
                                                                                            GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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Pred. No. 1.1e-18;
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Best Local Similarity 84.4%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: (256)..(3690)
US-10-428-817A-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Mus musculus
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Page 10

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Sequence 1477, Application US/10305720
Publication No. US20040010136A1
Publication No. US20040010136A1
APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression TILE REFERENCE: PA.0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: 09/016,434
PRIOR APPLICATION NUMBER: 09/016,434
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence 1, Application US/10475049A

publication No. US2055019854A1

GENERAL INFORMATION:

APPLICANT: Gross, Rene
APPLICANT: Lajoix, Anne-Dominique
APPLICANT: Ribes, Gerard
TITLE OF INVENTION: Novel Method For Screening Inhibitors of
TITLE OF INVENTION: Associated Protein and the Protein Inhibiting Neuronal
TITLE OF INVENTION: Associated Protein and the Protein Inhibiting Neuronal
TITLE OF INVENTION: NUMBER: US/10/475,049A
CURRENT APPLICANTON NUMBER: PS/10/475,049A
CURRENT FILING DATE: 2002-04-17
PRIOR FILING DATE: 2002-04-17
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 106
SEQ ID NO 1

SEQ ID NO 1

LENGTH: 4290

TENGTH: A290

TENGTH: A290

TENGTH: A290

TENGTH: A290

TENGTH: A290

TENGTH: A290
971 GGCTACCAGATGCCCGATGGCACCATCAGAGGGGATGCTGCCACCTTGGAGTTCACCCAG 1030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
OTHER INFORMATION: GenBank ID No. US20040010136A1 g951318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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US-10-305-720-1477
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LENGTH: 4079
TYPE: DNA
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US-10-631-467-1064

US-10-631-467-1064

Sequence 1064, Application US/10631467

Publication No. US2005208496A1

GENERAL INFORMATION:

APPLICANT Genox Research Inc.

TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive F

TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive F

TITLE OF INVENTION: MUMBER: US/10/631,467

CURRENT FILING DATE: 2003-07-31

PRIOR FILING DATE: 2003-07-31

PRIOR FILING DATE: 2002-03-20

PRIOR PELING DATE: 2002-08-06

NUMBER OF SEQ ID NOS: 2086

SEQ ID NO SEQ ID NOS: 2086

SEQ ID NO 1064

LENTH: 3991
                                                                                                                                                       APPLICANT: Genox Research Inc.
TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive justice of INVENTION: disease
FILE OF INVENTION: disease
FILE REPERBNCE: 3462.1005-000
CURRENT APPLICATION NUMBER: US/10/631,467
CURRENT APPLICATION NUMBER: US/203-077212
PRIOR PILING DATE: 2003-03-20
PRIOR PILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 208-06
NUMBER OF SEQ ID NOS: 208-06
SOFTWARE: Patentin version 3.1
SEQ ID NO 966
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Pred. No. 1.1e-18;
0; Mismatches 19; Indels
                                                                             Sequence 966, Application US/10631467
Publication No. US20050208496A1
GENERAL INFORMATION:
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Best Local Similarity 84.4%;
Matches 103; Conservative
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Matches 103; Conservative
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1 ORGANISM: Mus musculus
US-10-631-467-966
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CORGANISM: Mus musculus
US-10-631-467-1064
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121 GT 122
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US-10-305-720-1234
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                                                                                                                                                                                  Gaps
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PUBLICATION NO. US20050228172A9

GENERAL INFORMATION:

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: USCOLOGE POLYMORPHISMS in the Human Genome
FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US 60/255,065A

CURRENT FILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16
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                                                                                                                                Length 4290;
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                                                                                                                                                                                  29; Indels
                                                                                                                                  Score 75.6; DB 8;
Pred. No. 1.2e-13;
0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-889-121-8
; Sequence 8, Application US/10889121
; Publication No. US20040253685A1
                                                                                                                                       29.3%;
                                                                                                                                    Query Match
Best Local Similarity 76.21
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 66.4
Matches 81; Conservative
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US-09-925-065A-56987
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(4287)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1510 AT 1511
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US-09-925-065A-56987
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LENGTH: 700
                                                                                           US-10-475-049A-1
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GENERAL INFORMATION:
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TITLE OF INVERTION: Composition for the Detection of Signaling Pathway Gene Expressivente PRICATION VUMBER: US/10/305,720
CURRENT APPLICATION VUMBER: US/10/305,720
CURRENT FILING DATE: 1098-01-36
PRIOR APPLICATION NUMBER: 09/016,434
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL PROGram
SEQ ID NOS: 1490
APPLICANT: Sessa, William C.
TITLE OF INVENTION: BAOS MUTATIONS USEFUL FOR GENE THERAPY AND THERAPEUTIC SCREENING
TITLE OF INVENTION: BAOS MUTATIONS USEFUL FOR GENE THERAPY AND THERAPEUTIC SCREENING
TITLE OF INVENTION: 044574-5046-01
CURRENT APPLICATION NUMBER: US 09/956,699
PRIOR APPLICATION NUMBER: PCT/USO0/09913
PRIOR FILING DATE: 2000-00-14
PRIOR FILING DATE: 1999-04-16
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.2
SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3612;
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; OTHER INFORMATION: GenBank ID No. US20040010136A1 g189259
US-10-305-720-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 54.8; DB 8;
Pred. No. 3.7e-07;
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Best Local Similarity 65.6
Matches 80; Conservative
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Best Local Similarity
Matches 80; Conserva
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RESULT 40
US-10-889-121-9
Sequence 9, Application US/10889121
Sequence 9, Application US/10889121
Sequence 9, Application No. US20040253685A1
GENERAL INFORMATION:
APPLICANT: Sessa, William C.
TITLE OF INVENTION: eNOS WUTATIONS USEFUL FOR GENE THERAPY AND THERAPEUTIC SCREENING
FILE REFERENCE: 044574-5046-01
CURRENT APPLICATION NUMBER: US/10/889,121
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                                                                                                                                           803 GGCTACCGGCAGCAGCACGCTCTGTGCGGGGACCCAGCCAACGTGGAGATCACGAG
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APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REPERENCE: 9301-186-99
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/299,918
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
PRIOR PLICATION NUMBER: 10/172,118
PRIOR FILING DATE: 2002-06-14
PRIOR PLING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 414
                                                                                               1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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Score 54.8; DB 6; Length 4077; Pred. No. 3.7e-07; 0; Mismatches 42; Indels 0;
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Pred. No. 3.7e-07;
0; Mismatches 42;
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APPLICANT: He, Yudong
APPLICANT: Linsley, Peter S.
APPLICANT: Mao, Mao, Mao
APPLICANT: Roberts, Christopher J.
APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Van de Vijver, Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 414, Application US/10342887
Publication No. US20040058340A1
  Query Match
Best Local Similarity 65.6%;
Matches 80; Conservative (
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21.2%;
Best Local Similarity 65.6%;
Matches 80; Conservative
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US-10-342-887-414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION
                                                                                                                                                                                                                                                                                 121 GT 122
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TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressic
FILE REFRENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720

CURRENT FILING DATE: 2002-11-26

PRIOR PLING DATE: 1998-01-30

NUMBER OF SEQ ID NOS: 1490

SOFTWARE: PERL Program

SEQ ID NO 1369

LENGTH: 4035
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APPLICANT: Bernards', Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REPERENCE: 9301-175-999
CURRENT APPLICATION NUMBER: US/10/172,118
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g434699
US-10-305-720-1369
                                                                                                                                        ; Sequence 1369, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
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Publication No. US20030224374A1
GENERAL INFORMATION:
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; DATABASE ACCESSION NUMBER: M93718
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Lineley, Peter
APPLICANT: Mao, Mao
APPLICANT: Roberts, Chris
APPLICANT: Van 't Veer, Laura
APPLICANT: Van de Vijver, Marc
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Best Local Similarity 65.6 Matches 80; Conservative
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                   837 CT 838
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US-10-305-720-1369
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LENGTH: 4077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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CURRENT FILING DATE: 2004-07-12
PRIOR APPLICATION NUMBER: US 09/956,699
PRIOR FILING DATE: 2001-09-20
PRIOR PILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-04-14
PRIOR PILING DATE: 1090-04-16
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Version 3.2
LENGTH: 4077
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-889-121-9
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November 2005

available for processing searches. generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now

applications make up the Published_Applications_Main databases. Newly published applications will appear in the Published_Applications_New databases; older published

:rapbm (Published_Applications_AA_Main) and .rapbn (Published_Applications_AA_New) Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_Main) and .rnpbn (Published_Applications_NA_New). Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions I HIS PAGE BLANK (USPTO)

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Sequence 837, App
Sequence 43745, A
Sequence 318, Appl
Sequence 31860, A
Sequence 62600, A
Sequence 67, Appl
Sequence 67, Appl
Sequence 67, Appl
Sequence 671, Appl
Sequence 671, Appl
Sequence 671, Appl
Sequence 688, Appl
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Sequence 74, Appl
Sequence 3, Appli
Sequence 60778, A
                                                                                                                December 13, 2005, 16:32:55; Search time 238 Seconds (without alignments) 405.271 Million cell updates/sec
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                                                                                                                                                                                                                                      1 cageggagtgatggcaagca.....ttgttccccagctgtgcatc 258
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Sequence
Sequence
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Sequence 4
Sequence 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Applications NA New:*

1: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

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8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

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10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-11-121-086-74
US-10-750-185-60778
US-10-750-185-837
US-10-750-185-8375
US-11-112-908-38
US-10-750-185-62600
US-10-750-185-62600
US-11-121-086-67
US-11-121-086-67
US-11-121-086-86
US-11-121-086-86
US-11-121-085-868
US-10-750-185-8551
US-10-750-185-868
US-10-750-185-868
US-10-750-185-868
US-10-750-185-868
US-10-750-185-868
US-10-750-185-94914
US-10-750-185-94914
US-10-750-185-94914
US-10-750-185-14965
US-10-750-185-14965
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                                                                                                                                                                                                                                                                                                                                          3392430 seqs, 186927314 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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258
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Perfect score:
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Sequence 6, Appli	Sequence 11, Appl	Sequence 26897, A	Sequence 61399, A	Sequence 56711, A	Sequence 33, Appl	Sequence 551, App	Sequence 44988, A	Sequence 483, App	Sequence 67, Appl	Sequence 66, Appl	Sequence 39, Appl	Sequence 1, Appli	Sequence 49, Appl	Sequence 48, Appl	Sequence 52, Appl	Sequence 66, Appl	Sequence 47, Appl	Sequence 20492, A	Sequence 32804, A	Sequence 381, App	Sequence 1, Appli
US-10-645-441-6	US-10-645-441-11	US-10-750-185-26897	US-10-750-185-61399	US-10-750-185-56711	US-10-392-234A-33	US-10-821-234-551	US-10-750-185-44988	US-10-131-826A-483	US-11-080-991-67	US-11-121-086-66	US-11-112-908-39	US-10-496-711-1	US-11-112-908-49	US-11-112-908-48	US-11-112-908-52	US-11-121-086-66	US-11-112-908-47	US-10-750-185-20492	US-10-750-185-32804	US-10-131-826A-381	US-11-121-086-1
9	9	9	9	9	9	9	9	9	7	7	7	9	7	_	7	7	7	9	9	9	7
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10	10	10	2	10	10	10	10	2	5	10	2	10	2	2	2	10	10	10	10	5	10
28.2	28.2	28.2	28.2	28	28	27.8	27.8	27.8	27.8	27.8	27.8	27.6	27.6	27.6	27.6	27.6	27.6	27.4	27.4	27.4	27.4
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ALIGNMENTS

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WEILLIAFTONDALE, 1994

WEILLIAFTONDALE, 1994

WEILLIAFT COHEN, Daniel

APDICANT: Othen, Daniel

APDICANT: Dunmended, Marta

APDICANT: Blain, Bernard

APDICANT: Blain, Bernard

APDICANT: Baslouw, Laurent

BRIOR FILING DATE: 1999-10-12

BRIOR PILING DATE: 1999-10-13

BRIOR PILING DATE:
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2

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Sequence 3, Application US/11121086; Publication No. US20050266459A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 74
LENGTH: 154452
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 168516
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US-11-121-086-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                           122 TACCCGCCCCAGCCTCAGCCRCCGGCCATTGGGGCGGGGGGCGCCCGTGGTGAGCGAGTGA 181
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LOCATION: 1842..1862
OCHER INFORMATION: downstream amplification primer, complement
PEATURE:
                                                                                                                                                                                                                                                                                                                     Query Match 12.7%; Score 32.8; DB 7; Length 3001; Best Local Similarity 51.4%; Pred. No. 1.7; Matchés 76; Conservative 0; Mismatches 72; Indels 0
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Pred. No. 2.4;
0; Mismatches 123; Indels 0
                                          FEATURE:
NAME/KEY: misc_binding
LOCATION: 1502..1520
OTHER INFORMATION: 99-26223-225.mis2, complement
                                                                                                    FEATURE:
NAME/KEY: primer_bind
LOCATION: 1277..1297
OTHER INFORMATION: upstream amplification primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 CAGAGTGGAGCCCAGAGGAGACACGCAG 209
                                                                                                                                                                                                                                          NAME/KEY: misc_binding
LOCATION: 1489..1513
OTHER INFERMATION: 99-26223-225 probe
US-11-145-703-194
                 LOCATION: 14817.1500
OTHER INFORMATION: 99-26223-225.mis1
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ORGANISM: Bovine 19866880650684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ucery match
Best Local Similarity 46.3%;
Matches 106; Conservative
NAME/KEY: misc binding LOCATION: 1481.1500
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117867 GCCCTGCGGCTGCCGCATGCCCTCGGGGTCGAGCGGACGGGGGGGCGCCGGGC 117926
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                                                                                                                                                                                                                                   1134 TGCTGGCTGTGCACCAGGCCTGGTCCAAGTGAGGCTGAGAAAGCTACAGCCGGGATGAG 1193
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82 AGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGGTACCCGGCCCAGCCTCAGCC 141
                                                                                                                                                         142 RCCGGCCATTGGGGCGGGGAGCCCCCGTGAGGAGTGACAGAGTGGAGCCCCAGAGGAG 201
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Publication No. US20050266459A1

GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
TILE REFERENCE: 0913946-000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR PILING DATE: 2004-05-04
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.3
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APPLICANT: INTOGNILLON:
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OP INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REPERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT APPLICATION NUMBER: US/11/121,086
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR PILING DATE: 2004-05-04
PRIOR FILING DATE: 2004-05-04
SOFTWARE: PALENTIN NUMBER: 05/507,570
SOFTWARE: PALENTIN NUMBER: 05/507,570
SOFTWARE: PALENTIN NUMBER: 05/507,570
SOFTWARE: PALENTIN NUMBER: 05/507,570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
12.0%; Score 31; DB 7; Length 154452;
Best Local Similarity 58.4%; Pred. No. 7.7;
Matches 52; Conservative 1; Mismatches 36; Indels 0
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66 CCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGGTACC 125
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i Sequence 43745, Application US/10750185

j Sequence 43745, Application US/10750185

j Publication No. US20050260603A1

j GENERAL INFORMATION:

APPLICANT: NOTISE, SUE K.

APPLICANT: ROSENPELD, David

APPLICANT: HOLM, Tom

APPLICANT: HOLM, Tom

APPLICANT: BATES, Stephen

TILLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

TILLE REPERENCE: MM1100-2

CURRENT APPLICATION HUMBER: US/10/750,185

CURRENT FILING BATE: 203-12-3/1
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                                                                                                                                                                                                                                                                                                                 Length 4745;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   752 CCGCCCAGCCTCAGGCCAAAGCTGTCTGGAGATCAGTCCCAGTGG 796
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                                                                                                                                                                                                                                                                                                                                                              56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6;
                                                                                                                                                                                                                                                                                                            Score 30; DB 6;
Pred. No. 10;
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Publication No. US20050260659A1
GENERAL INFORMATION:
APPLICAMT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/531,596
; PRIOR FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/562,417
; PRIOR FILING DATE: 2004-04-14
; NUMBER OF SEQ ID NOS: 2184
; SOFTWARE: FB&ESEQ for Windows Version 4.0
; SEQ ID NO 837
; LENGTH: 4745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 29.8;
Pred. No. 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SEQ ID NO 43745
LENGTH: 1678
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55.2%;
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Best Local Similarity 52.5%;
Matches 63; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                         , ORGANISM: H. sapiens
US-10-909-125-837
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                                                                                                                                                                                                                       TYPE: DNA
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APPLICANT: Jain, Raylishen
APPLICANT: Bhat, Balkrishen
APPLICANT: Brat, Balkrishen
APPLICANT: Bratla, Eigen
TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation
TITLE OF INVENTION: Of Small Non-Coding RNAs
FILE REPERENCE: ISISO008-100 (COREO016US)
CURRENT APPLICATION NUMBER: US/10/909,125
CURRENT FILING DATE: 2004-07-30
PRIOR PLILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: US 60/492,056
PRIOR APPLICATION NUMBER: US 60/516,303
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                                                                                                                                                                                                                                 Sequence 60778, Application US/10750185

Publication No. US20050260603A1

GENERAL INPORMATION:

APPLICANT: MAI GENOMICS, INC.

APPLICANT: DeNISE, Sue K.

APPLICANT: RESERR, Richard

APPLICANT: ROSENFELD, David

APPLICANT: HOLM, Tom

APPLICANT: BATES, Stephen

APPLICANT: FANTIN, Dennis

TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT APPLICATION NUMBER: US 60/437,482

PRIOR PILING DATE: 2003-12-31

NUMBER OF SEQ ID NOS: 64922

SOFTWARE: PALENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6; Length 2840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 11.9%; Score 30.6; DB 6; Length 2
Best Local Similarity 60.8%; Pred. No. 6.8;
Matches 48; Conservative 1; Mismatches 30; Indels
                                                                                                                            98331 gcadegerendeccacedeadeccacacecereacecr 98367
                                                                               181 ACAGAGTGGAGCCCAGAGACACGCAGCCCGGGCT
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Publication No. US20050261218A1
GENERAL INFORMATION:
APPLICANT: Beau, Christine
APPLICANT: Beau, Christine
APPLICANT: Bennett, C. Frank
APPLICANT: Ferier, Susan M.
APPLICANT: Griffey, Richard H.
APPLICANT: Baker, Brenda F.
APPLICANT: Warcuson, Eric G.
APPLICANT: Warcuson, Eric G.
APPLICANT: Koller, Erich
APPLICANT: Swayze, Eric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2295 ACAGATGGGAGCCCCGAGG 2277
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US-10-750-185-60778
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LENGTH: 2840
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APPLICANT:
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218 TACAGACTCACAGGCCCGTCTTGTTCCCCAGC 250
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US-10-750-185-31860
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US-10-750-185-62600
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Best Local Similarity
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                                                                                                                   셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12535 CCCACACGCCCGGCCGCCGCCCTCCCAGCTGGTCCACCCCGGCGGGGCCCGCGCCCC 12476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 CTCATCCGCTATGCTGGCTACCAGATGCCAGATGAGCAGCATCAGAGGGGACCCTGCCAAC 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           782 cricicaciones de contracertados de contraces de contr
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
FILE APPLICANT: FAUTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REPERENCE: MAILIOG-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 63750
LENGTH: 1009
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Pred. No. 17;
1; Mismatches 88; Indels
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FILE REFERENCE: 04-164-US
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT FILING DATE: 2005-04-22
PRIOR APPLICATION NUMBER: US 60/564,758
PRIOR APPLICATION NUMBER: US 60/55,978
PRIOR PILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR PILING DATE: 2004-10-60
PRIOR APPLICATION NUMBER: US 60/633,826
PRIOR FILING DATE: 2004-11-30
PRIOR PILING DATE: 2004-11-07
NUMBER OF SEQ ID NOS: 511
SOFTWARE: PATCHING DATE: 2004-12-07
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US-10-750-185-63750/c
US-10-750-185-63750, Application US/10750185
Publication No. US20050260603A1
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ORGANISM: Bovine 19866880851319
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APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 48.0 Matches 82; Conservative
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Best Local Similarity 49.0
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
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LENGTH: 171162
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64 TACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGGTA 123
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                                                                                                                               US-10-750-185-31860/c

| Sequence 31860, Application US/10750185
| Sequence 31860, Application US/10750185
| Publication No. US20050260603A1
| GENERAL INFORMATION:
| APPLICANT: MAI GENOMICS, INC.
| APPLICANT: MERR, Richard
| APPLICANT: KERR, Richard
| APPLICANT: ROBINFELD, David
| APPLICANT: BATES, Stephen
| APPLICANT: BATES, Stephen
| APPLICANT: POLMYIN, Dennis
| TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
| FILE REFERENCE: MMI1100-2
| CURRENT PLIJIG DATE: 2003-12-31
| PRIOR FILING DATE: 2003-12-31
| PRIOR FILING DATE: 2002-12-31
| SEQ ID NO 31860
| LENGTH: 1676
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GENERAL INFORMATION:
APPLICANT: MAI GENOMICS, INC.
APPLICANT: MAI GENOMICS, INC.
APPLICANT: MAI GENOMICS, INC.
APPLICANT: MAINATION:
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
FILE REPERBNCE: MAI1100-2
CURRENT ELINO NUMBER: US 60/437,482
FRICA APPLICATION NUMBER: US 60/437,482
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662 recreranceagecegeceragerececkée 630
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Publication No. US20050260603A1
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Publication No. US20050255114A1

GRNERAL INFORMATION:

GRNERAL INFORMATION:

APPLICANT: Black. Ivan

APPLICANT: Stache-Crain, Birgit

APPLICANT: Andarmani, Susan

APPLICANT: Andarmani, Susan

APPLICANT: Andarmani, Susan

APPLICANT: Andarmani, Susan

FILE REFERENCE: 821A

CURRENT APPLICATION: Whethods for Diagnosis and Treatment of Preeclampsia

FILE REFERENCE: 821A

CURRENT PAPLICATION NUMBER: US/10/821,234

CURRENT FILING DATE: 2004-04-07

FRIOR APPLICATION NUMBER: US 60/462,047

FRIOR FILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SEQ ID NO 671

SEQ ID NO 671
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Pred. No. 19;
                                                                                                131867 crgacrecrererecerragirrerec 131896
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                                  216 CTTACAGACTCACAGGGCCCGTCTTGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1665 GIGCCIGGAGCCCTGCAGGICTC 1687
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Best Local Similarity 50.4%;
Matches 71; Conservative (
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SOFTWARE: PatentIn version 3.3
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Best Local Similarity 49.7
Matches 71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Homo sapiens
US-10-821-234-671
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                                                                                                                                                                                                                                                  US-10-821-234-671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 67, Application US/11121086

Publication No. US2005026645941

GENERAL INFORMATION:

APPLICANT: POULSEN, TIM S.

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT APPLICATION NUMBER: 60/567,570

PRIOR APPLICATION NUMBER: 60/567,570

RIOR APPLICATION NUMBER: 60/567,570

RIOR APPLICATION NUMBER: 2004-05-04

NUMBER OF SEQ ID NOS: 107

SOFTWARE: PATENTIN OF 3.3

SEQ ID NO 67

LENGTH: 179666
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| Sequence 4, Application US/11121086
| Publication No. US20050266459A1
| GENERAL INFORMATION:
| APPLICANT: POULSEN, TIM S.
| APPLICANT: NIELSEN, KIRSTEN V.
| TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
| FILE REFERENCE: 09138.6000-00000
| CURRENT APPLICATION NUMBER: US/11/121,086
| CURRENT PILING DATE: 2005-05-04
| PRIOR PILING DATE: 2005-05-04
| PRIOR FILING DATE: 2004-05-04
| NUMBER OF SEQ ID NOS: 107
| SOFTWARE: Patentin version 3.3
| SEQ ID NO 4
                                                                         53 GCTATGCTGGCTACCAGATGCCAGATGCCAGCATCAGAGGGGACCCTGCCAACGTGGAAT 112
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 29.4; DB 7; Length 1 Pred. No. 22; 1; Mismatches 47; Indels
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42; Indels
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   1; Mismatches
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Best Local Similarity 54.3%;
Matches 57; Conservative
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       54; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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Matches 52; Conserv
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       Matches
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71; Indels

Length 3772;

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Sequence 20, Application US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR PILING DATE: 2004-05-04
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Pred. No. 27;
0; Mismatches
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Sequence 34965, Application US/10750185; Publication No. US20050260603A1; GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: MERR, Richard
APPLICANT: ROSENPELD, David
APPLICANT: ROSENPELD, David
APPLICANT: ROSENPELD, David
APPLICANT: RATES, Stephen
APPLICANT: FANTIN, Dennis
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 54914, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
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; ORGANISM: Bovine 19866881313891
US-10-750-185-54914
ORGANISM: Bovine 19866880936088
                                                                      Query Match 11.2%;
Best Local Similarity 54.8%;
Matches 57; Conservative
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       ; OKGANISM: DOVING
US-10-750-185-56551
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108108 CTCAGCCCCTCACCTGGCAGCCTGTTGCCCTGTGCCCCTCAGTGAGGAGACGGAGGTCAT 108049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: GENORISE, Sue K.
APPLICANT: GENORISE, Sue K.
APPLICANT: RERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: RATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: RANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
CURRENT PILING DATE: 2003-12-31
PRIOR FILING DATE: 2003-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE PAFFENTIN VERSION 3.1
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Publication No. US20050260603A1
                                                                                                                                                                                                                                                                                                                  Sequence 868, Application US/10750185
Publication No. US20050260603A1
                                                                                                                                                CGTGGTGAGCGAGTGACAGAG 186
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Best Local Similarity 56.7%;
Matches 51; Conservative
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APPLICANT: WAI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Bovine MMBT07408
US-10-750-185-868
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US-10-750-185-56551/c
                                                                                                                                                                                                                                                                    RESULT 16
US-10-750-185-868/c
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LENGTH: 1564
TYPE: DNA
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1394 GCGGGTGGCCTGGGGCTGAGGGGGATGGATGACCTGAGGGGGCTTCCAGGTGGG 1335
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                                                                                                                              155 GCGGGGAGCCCCGTGGTGAGCGAGTGACAGAGTGGAGCCCCAGAGGAGACACGCCGGG
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Score 28.8; DB 6; Length 1564;
Pred. No. 20;
0; Mismatches 47; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 11.1%; Score 28.6; DB 6; Length 861; Best Local Similarity 55.6%; Pred. No. 22; Matches 55; Conservative 0; Mismatches 44; Indels
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APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
FITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR PELING DATE: 2003-12-31
                                                                                                                                                                                                                                                                                                         1334 GCTGAGGGCCTGAAGGGGACCATCTTGTCTACCTGAGGTTCCTC 1291
                                                                                                                                                                                                                                              215 GCTTACAGACTCACAGGGCCCGTCTTGTTCCCCCAGCTGTGCATC 258
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NUMBER OF SEQ ID
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Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: POULSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-00.04
PRIOR FILING DATE: 2005-00.04
PRIOR FILING DATE: 2004-05-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMILLOO-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT PILIG DATE: 2003-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 25939
LENGTH: 1543
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Pred. No. 22;
                                                                                                                                                                                           1; Mismatches
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Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25939, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
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Best Local Similarity 53.2%;
Matches 58; Conservative
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les 58; Conservative
                                                                           TYPE: DNA
CRGANISM: Bovine
US-10-750-185-34965
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US-10-750-185-25939
NUMBER OF SEQ ID N
SOFTWARE: PatentIN
SEQ ID NO 34965
LENGTH: 1196
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APPLICANT:
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APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
GURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
FRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 45463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.0%; Score 28.4; DB 6; Length 2335; 48.2%; Pred. No. 27;
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Pred. No. 36;
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US-10-750-185-45463
; Sequence 45463, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: ROSENFELD, David
: APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/11121086 Publication No. US20050266459A1 GENERAL INFORMATION:
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                                                                                                                                                                    11.1%;
50.8%;
version 3.3
                                                                                                                                                                                                                 90; Conservative
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                                                                         TYPE: DNA ORGANISM: Homo sapiens
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Matches 80; Conserv
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SOFTWARE: Patentin
SEQ ID NO 105
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                                             LENGTH: 171486
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US-11-121-086-6/c
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176S GAGCGAACTGTCAGGCAGGACAGGAÁGÁTGGTGAAACCAÁGGGCÁAAGAGGGGCCTGGCGT 1706
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                               158 GGGAGCCCCGTGGTGAGCGAGTGACAGAGTGGAGCCCAGAGGAGACACGCAGCAGCCGGGCT 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang, Yifeng
The Regents of the University of California
The Government of the United States of America
as represented by the Secretary of the
Department of Health and Human Services
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Mammalian Sweet Taste Receptors
FILE REFERENCE: 02307E-120110US
CURRENT APPLICATION NUMBER: US/10/645,441
CURRENT FILING DATE: 2003-08-20
PRIOR APPLICATION NUMBER: US/09/927,315
PRIOR APPLICATION NUMBER: US 60/302,898
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-07-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: mouse T1R2 sweet taste receptor
US-10-645-441-11
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                                                                                                                                218 TACAGACTCACAGGGCCCGTCTTGTTCCCCA
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Publication No. US20050260603A1
Publication No. US20050260603A1
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, SUR K.
APPLICANT: RERR, Richard
APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/10645441 Publication No. US20050260599A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Nelson, Greg
Hoon, Mark A.
Chandrashekar, Jayaram
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Zuker, Charles S. APPLICANT: Ryba, Nicholas J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Mus musculus
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US-10-750-185-26897/c
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 GCGAGTGACAGAGTGGAGCCCAGAGGAGACACGCAGCCCGGGCTTACAGACTCACAGGGC 233
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APPLICANT: POULSEN, TIM S.

APPLICANT: NELSEN, KTRSTEN V.

TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES FILE OF INVENTION: NUCLEIC ACID PROBES FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR APPLICATION NUMBER: 60/567,570
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Zhang, Yifeng
APPLICANT: The Regents of the University of California
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Mammalian Sweet Taste Receptors
FILE REFERENCE: 02307E-120110US
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 21; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/645,441 CURRENT FILING DATE: 2003-08-20
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PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/302,898
PRIOR FILING DATE: 2001-07-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zuker, Charles S.
APPLICANT: Ryba, Nicholas J.P.
APPLICANT: Nelson, Greg
APPLICANT: Hoon, Mark A.
APPLICANT: Chandrashekar, Jayaram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/10645441 Publication No. US20050260599A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 45.5.
Thea 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 66.1
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                     SEQ ID NO 6
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SEQ ID NO 33
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Best Local
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US-10-750-185-61399/C
Sequence 6.1399, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: MMI GENOMICS, INC.
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: BAYTIN, Dennis
TILLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT APPLICATION NUMBER: US (0/437,482)
PRIOR APPLICATION NUMBER: US (0/437,482)
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SEQ ID NO 61399
TYPE: NANA
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0
HAPPLICANT: HOLM, Tom
HAPPLICANT: BATES, Stephen
HAPPLICANT: BATES, Stephen
HAPPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MAIL100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
HALOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 26897
LENGTH: 3745
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Pred. No. 33;
1; Mismatches
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US-10-750-185-56711
Sequence 56711, Application US/10750185
; Publication No. US20050260601A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Bovine 19866880721875
US-10-750-185-26897
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llarity 70.6%;
Conservative 1
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Best Local Similarity 52.1%;
Matches 63; Conservative
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Best Local Similarity
Matches 36; Conserv
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US-10-750-185-61399
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APPLICANT: Buxer, Steven
APPLICANT: Poole, Keith
APPLICANT: Poole, Keith
APPLICANT: Poole, Keith
APPLICANT: Decker, Duglas
APPLICANT: Decker, Duglas
APPLICANT: Maznhi ii
TITLE OF INVENTION: Method for Screening for acrAB Transporter Family Inhibitors
FILE REPERENCE: 6206
CURRENT APPLICATION NUMBER: US/10/392,234A
CURRENT FILING DATE: 2003-03-17
PRIOR PILING DATE: 2003-03-15
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin version 3.1
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Pred. No. 33;
1; Mismatches 66; Indels
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                                                      APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stembes
APPLICANT: FANTIS, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MAILION-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
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; Sequence 33, Application US/10392234A
; Publication No. US20050255538A1
; Publication No. US20080255538A1
; Publication Poparmacia and Upjohn Corporation
                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Bovine 19866880824999
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1 Similarity 47.7%;
82; Conservative (
                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
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Best Local Similarity 50.0%;
Matches 67; Conservative
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DeNISE, Sue K.
KERR, Richard
ROSENFELD, David
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                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 56711
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APPLICANT: Zhang, Zemin

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C128

CURRENT APPLICATION NUMBER: US/10/131,826A

CURRENT FILING DATE: 1997-06-18

PRIOR PELING DATE: 1997-06-18

PRIOR PELING DATE: 1997-06-18

PRIOR PELING DATE: 1997-09-17

PRIOR PELING DATE: 1997-09-18

PRIOR PELING DATE: 1997-09-18

PRIOR PELING DATE: 1997-09-18

PRIOR PELING DATE: 1997-09-19

PRIOR PELING DATE: 1997-09-19
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                                                         1440 Argagracaadgraccraagtrecredecrrecedarecereaceaegraagaarere 1381
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20 ACGACTICCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGATGCCAGATG
                                                                                                                   80 GCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAGGTACCCGGCCCCAGCCTCAG
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Pred. No. 40;
1; Mismatches
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Sequence 483, Application US/10131826A
Publication No. US20050245730A1
GENERAL INPORMATION:
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Best Local Similarity 54.6%;
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stewart, Timothy A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumas, Daniel
Watanabe, Colin K
Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Godowski, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sherwood, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo Sapien
US-10-131-826A-483
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APPLICANT:
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                                                                                                                                                                                                                                                          Sequence 551, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION:
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234

CURRENT PILING DATE: 2004-04-07

PRIOR FILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: pt_SEQ_genes Version 1.0

SEQ ID NO 551

LENGTH: 792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            303 CCTGGCCCAGGTGGACGTGCAGAACCGCCTGAAGAAAGCCGAGGCGCGCATGCCGCAGGC 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                         201 GACACGCAGCCCGGGCTTACAGACTCACAGGGCCCGTCTTGTTCCCCCAGCTG 252
                                                                                                                   363 Gerecreaccasescricaserceascasacasesces de 114
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APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMILLIOG-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PAGE ID NOS: 64922
SOFTWARE: PAGE ID NOS: 64922
LENGHH, 2233
LENGHH, 2233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 10.8%; Score 27.8; DB 6; Length 792; Best Local Similarity 54.6%; Pred. No. 36; Matches 53; Conservative 1; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 AGACACGCAGCCCGGGCTTACAGACTCACAGGGCCCG 236
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Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: RERR, Sichard
APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Bovine 19866880984581
US-10-750-185-44988
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Matches 68; Conservative
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CORGANISM: Homo sapiens
US-10-821-234-551
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Sequence 1, Application US/10496711

Sequence 1, Application No. US20050256649A1

Publication No. US20050256649A1

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHIC FORMS WITH MULTIPLE PHENOTYPES WITHIN CLINICAL

TITLE OF INVENTION: POPULATIONS
FILE REPERENCE: PU4699W0

CURRENT APPLICATION NUMBER: US/10/496,711

CURRENT PILING DATE: 2004-05-26

PRIOR PAPLICATION NUMBER: 60/344992

PRIOR PLING DATE: 2002-12-21

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PRACESO for Windows Version 4.0

SEQ ID NO 1

LENGTH: 2085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 10.8%; Score 27.8; DB 7; Length 179892; al Similarity 54.6%; Pred. No. 59; 53; Conservative 1; Mismatches 43; Indele A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Harris, Cole
APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REFERENCE: 04-164-US
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT APPLICATION NUMBER: US 60/564,758
PRIOR APPLICATION NUMBER: US 60/575,978
PRIOR FILING DATE: 2004-04-23
PRIOR FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR PILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-12-07
NUMBER OF SEQ ID NOS: 511
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                         Sequence 39, Application US/11112908; Publication No. US20050260659A1; GENERAL INFORMATION:
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Best Local Similarity 56.7
Matches 51; Conservative
                                                                                                                    127 GGCCCAGCCTC 137
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; ORGANISM: Homo Sapiens
US-10-496-711-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                             US-11-112-908-39/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Fublication No. US20050266437A1
GENERAL INFORMATION:
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: LOBY, PETER OF INVENTION: AND OVARIAN CANCER
TITLE OF INVENTION: AND OVARIAN CANCER
TITLE OF INVENTION: AND OVARIAN CANCER
TITLE APPLICATION NUMBER: US/11/080,991
CURRENT FILING DATE: 2005-03-11
FRIOR APPLICATION NUMBER: US/10/176,847
PRIOR FILING DATE: 2005-06-21
NUMBER OF SEQ ID NOS: 112
SOUTHWARE: FASTESQ for Windows Version 4.0
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   93 CCATGGGCTCGGGGAACCCCGGGGCCCGGTGTTTGCTGGCTCCAGGAGGCCAGGAGG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 GGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGGTACCCGGCCCAGCCTCA 138
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APPLICANT: POULSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6.000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR PRIJING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PATENTIN VERSION 3.3
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                                                                                                                                                                                              153 ccaccrecaeccreerecrecaeacrearereacee 189
                                                                                                                        200 AGACACGCCCGGCCTTACAGACTCACAGGCCCCG 236
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Publication No. US20050266459A1
GENERAL INFORMATION:
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US-11-121-086-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
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LENGTH: 163162
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US-11-121-086-66
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98554 AAGCAACGCCCCGGGGCGACCGGCTCGTTGCTGCGGCGCCCACGCAAGCCGAAACCGAT 98495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 TCAGCCRCCGCCCATTGGGGCGGGGAGCCCCGTGGTGACGGGTGACAGAGTGGAGCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 AAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGATGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                           Score 27.6; DB 7; I Pred. No. 67; 1; Mismatches 105;
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Pred. No. 67;
1; Mismatches 105;
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Publication No. US2005026659A1
GENERAL INFORMATION:
APPLICANT: Harris, Cole
APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REFERENCE: 04-164-US
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT FILING DATE: 2005-04-22
PRIOR FILING DATE: 2004-04-23
PRIOR FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US 60/55,978
PRIOR FILING DATE: 2004-11-30
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-07
NUMBER OF SEQ ID NOS: 511
SCOFWARE: PATCHIN VERBION 3.3
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR FILING DATE: 2004-11-30
PRIOR APPLICATION NUMBER: US 60/633,826
PRIOR FILING DATE: 2004-12-07
NUMBER OF SEQ ID NOS: 511
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98374 Gráchaccracacaca 98359
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ilarity 45.9%;
Conservative
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Best Local Similarity 45.94
Matches 90; Conservative
                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 90; Conservat
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SEQ ID NO 52
LENGTH: 161726
                                                                                                                                                                                                                                   LENGTH: 161726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-11-112-908-52/c
                                                                                                                                                                                                                                                                                                                            US-11-112-908-48
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                                                                                                  1572 cdácccadactecentecadantentadadeceadadecreacecendedeceadaden 1513
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                                          126 CGGCCCAGCCTCAGCCRCCGGCCATTGGGGCGGGGAGCCCCGTGGTGAGCGAGTGACAGA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 AAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGATGCCA 75
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                                                                                                                                                                                                                                                                                                                                                                              Sequence 49, Application US/11112908
Publication No. US20050260659A1
GENERAL INPORMATION:
GENERAL INPORMATION:
TITLE OF INVENTION:
FILE REFERENCE: 04-164 US
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT FILING DATE: 2005-04-22
FRIOR FILING DATE: 2004-04-23
FRIOR APPLICATION NUMBER: US 60/564,758
FRIOR APPLICATION NUMBER: US 60/575,978
FRIOR FILING DATE: 2004-13
FRIOR FILING DATE: 2004-11-30
FRIOR FILING DATE: 2004-11-30
FRIOR FILING DATE: 2004-11-07
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APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REPERENCE: 04-164-US
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT FILING DATE: 2005-04-22
PRIOR FILING DATE: 2004-04-23
PRIOR FILING DATE: 2004-04-23
PRIOR FILING DATE: 2004-06-01
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Publication No. US20050260659A1
GENERAL INFORMATION:
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Matches 90; Conserv
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US-11-112-908-49/c
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                                                                                                                                                                                                       US-11-11-08-08-06-05

| Josephence 66, Application US/11121086
| Publication No US20050266459A1 |
| GENERAL INFORMATION |
| APPLICANT: POULSEN, TIM S. |
| APPLICANT: NIELSEN, KIRSTEN V. |
| TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES |
| TILE REFERENCE: 09138.600-000000 |
| CURRENT APPLICATION NUMBER: US/11/121,086 |
| CURRENT APPLICATION NUMBER: 06/567,570 |
| PRIOR FILING DATE: 2004-05-04 |
| NUMBER OF SEQ ID NOS: 107 |
| SOFTWARE: PatentIn version 3.3 |
| SOFTWARE: PatentIn version 3.3 |
| TIPE: DNA |
| TIPE: DNA |
| ORGANISM: Homo sapiens |
| US-11-121-086-66 |
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Best Local Similarity 51.6%; Pred. No. 67;
Matches 63; Conservative 0; Mismatches 59; Indels 0;
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US-11-121-086-66/c
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Sequence:

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Sequence 58299, A Sequence 267621, Sequence 267622, Sequence 14604, A Sequence 14606, A Sequence 170140, Sequence 52023, Sequence 520337, Sequence 520337, Sequence 271334, Sequence 271334, Sequence 271334, Sequence 271334,
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Sequence 336028,
Sequence 368993,
Sequence 372996,
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Sequence 523844, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REPERENCE: 365-01.
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Pasha, Abdul Qadar Mohammad
APPLICANT: Pasha, Abdul Qadar Mohammad
APPLICANT: Ahsan, Aarif
TITLE OF INVENTION: A method of detection of predisposition
TITLE OF INVENTION: to high altitude pulmonary edema (HAPE)
FILE REFERENCE: 09755-0018US1
CURRENT APPLICATION NUMBER: US/10/713,137
CURRENT FILING DATE: 2003-11-13
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 24; DB 9; Length 24; 100.0%; Pred. No. 0.38;
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US-10-719-956-198953
US-10-719-906-58299
US-10-719-900-267621
US-10-719-900-267621
US-10-719-900-267622
US-10-956-157-14604
US-10-956-157-14604
US-11-036-317-189892
US-11-036-317-189892
US-11-036-317-59992
US-11-036-317-59992
US-11-036-317-59992
US-10-719-900-520333
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US-11-036-317-183105
US-11-036-317-27344
US-11-036-317-272728
US-11-036-317-316163
US-11-036-317-336028
US-11-036-317-372996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                         24; Conservative
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Matches 24; Conser
     RESULT 2
US-11-036-317-523844
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     SEQ ID NO 3
LENGTH: 24
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Sequence 683762,
Sequence 83698, A
Sequence 743593,
Sequence 904575,
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                                                                                                                                       December 13, 2005, 13:21:57; Search time 660 Seconds (without alignments) 300.705 Million cell updates/sec
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/ (gn2 6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/ (gn2 6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*
/ (gn2 6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
/ (gn2 6/ptodata/1/pubpna/USIOA_PUBCOMB.seq:*
/ (gn2 6/ptodata/1/pubpna/USIOB_PUBCOMB.seq:*
                           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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0 US-11-036-317-296939

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US-10-874-242-35

US-10-719-900-741411

US-10-719-900-741411

US-10-719-900-81215

US-10-809-189-2895

US-10-719-900-599645

US-10-956-157-14605

US-10-956-157-14605

US-10-719-956-2771

US-10-719-956-2771

US-10-719-956-2771

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US-10-719-956-28955

US-10-719-956-2771

US-10-719-956-28955
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US-10-719-956-663762
US-10-719-900-83698
US-10-719-900-743593
US-10-719-900-904575
US-10-719-900-909803
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Maximum Match 100%
Listing first 45 summaries
                                                                                                   - nucleic search, using sw model
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24
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Match Length
                                                                                                                                                                                                                                                                                                IDENTITY NUC
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US-10-719-900-979803/c
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US-10-719-956-683762/c

; Sequence 683762, Application US/10719956
; Publication No. US20040146910A1
; GENBEAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REPERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENOTH: 25
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Sequence 83698, Application US/10719900

Publication No. US2005026164A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION Methods of Genetic Analysis of Mouse

FILE REFERENCE: 3528.1

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,808

FRIOR FILING DATE: 2003-11-20

NUMBER OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 83698

LENGTH: 25

TUBER OF SEQ ID NOS: 982914

SEQ ID NO 83698
                                                                                                                      Length 25;
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                                                                                                                  Query Match 70.0%; Score 16.8; DB 10; Best Local Similarity 90.0%; Pred. No. 8e+02; Matches 18; Conservative 0; Mismatches 2;
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                                                                                                                                                                                                                              6 GCTGCACAGCTGAGGAACAA 25
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US-10-719-956-683762
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Matches 17; Conservative
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                                        TYPE: DNA
CORGANISM: Mus musculus
US-11-036-317-523844
; SEQ ID NO 523844
; LENGTH: 25
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                     LENGTH:
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; Sequence 979803, Application US/10719900
; Publication No. US200026164A1
; CENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; TITLE OF INVENTION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2002-11-20
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 979803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 904575, Application US/10719900
; Sequence 904575, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; TITLE OF INVENTION: WIMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2002 11 20
; RUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 904575
; LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                   Length 25;
                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Micrarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 743593
LENGTH: 25
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                                                             APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR FILING DATE: 2003-11-20
PRIOR FILING DATE: 2002 11 20
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Pred. No. 2.3e+03;
0; Mismatches 2;
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Pred. No. 2.3e+03;
0; Mismatches 2;
; Sequence 743593, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
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Best Local Similarity 89.5$
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Best Local Similarity 89.5.
Best Local 7; Conservative
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CORGANISM: Mus musculus
US-10-719-900-904575
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US-10-719-900-743593
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; Sequence 741411, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Mus musculus
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US-10-874-242-35
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TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse FILE REFERENCE: 3654.11
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR PAPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SEQ ID NO 296939
LENGTH: 25
LENGTH: 25
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APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT APPLICATION NUMBER: US 60/536,639
PRIOR APPLICATION NUMBER: US 60/536,639
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10; Length 25;
                                                                                                   Score 15.8; DB 8; Length 25; Pred. No. 2.3e+03; 0; Mismatches 2; Indels
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Best Local Similarity 81.8%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 4
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Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 498568, Application US/11036317 Publication No. US20050214823A1 GENERAL INFORMATION:
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                                                                                                                                                                                        4 GCACAGCTGGGGAACAAGA 22
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                                                                                                      Query Match
Best Local Similarity 89.5%;
Matches 17; Conservative
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US-11-036-317-296939
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                   ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-979803
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LENGTH: 25
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; OTHER INFORMATION: forward primer for amplifying beta-actin promoter containing; OTHER INFORMATION: intron 1
US-10-874-242-35
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Sequence 810975, Application US/11036317
; Sequence 100975, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
    APPLICANT: Blume, John
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; TITLE OF INVENTION: MAMBER: US/11/036,317
; CURRENT PILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; FRIDR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; ENDING 810975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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TITLE OP INVENTION: Methods of Genetic Analysis of Mouse
FILE REPERBICE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: EXPENS, SCOTT
APPLICANT: ZHANG, WEIQUN
TITLE OF INVENTION: NOVEL PROMOTERS AND USES THEREOF
FILE REFERENCE: 07580.0027-00000
CURRENT APPLICATION NUMBER: US/10/874,242
CURRENT FILING DATE: 2004-06-24
PRIOR APPLICATION NUMBER: 60/480,768
PRIOR APPLICATION NUMBER: 60/480,768
PRIOR APPLICATION NUMBER: 2003-06-24
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.2
SEQ ID NO 35
LENGTH: 26
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US-10-719-900-599645
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LENGTH: 25
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| Publication No. US20050026164A1
| GENERAL INFORMATION:
| APPLICANT: We Mei Zhou
| TITLE OF INVENTION: Methods of Genetic Analysis of Mouse;
| TITLE OF INVENTION: Wethods of Genetic Analysis of Mouse;
| CURRENT APPLICATION NUMBER: US/10/719,900
| CURRENT FILING DATE: 2003-11-20
| PRIOR FILING DATE: 2002-11-20
| NUMBER OF SEQ ID NOS: 982914
| SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
| LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.3%; Score 15.2; DB 8; Length 25; 85.0%; Pred. No. 4.4e+03;
                                                                                                                                                                                                                               63.3%; Score 15.2; DB 8; Length 25; 85.0%; Pred. No. 4.4e+03;
               PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 71411
LENGTH: 25
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; Publication No. US20050048531A1
GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; TTLLE OF INVENTION: Mcthods of Genetic Analysis
; TILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 06/100,678
; PRIOR APPLICATION NUMBER: 60/100,678
; RILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFWARE: FEBLENCE OF Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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2003-11-20
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Matches 17; Conservative
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; ORGANISM: mus musculus
US-10-809-189-92895
                                                                                                                                               ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-741411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-841215
CURRENT FILING DATE:
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US-10-719-900-841215/c
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LENGTH: 25
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; Sequence 223845. Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Bllume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3664.1
; CURRENT PRILICATION NUMBER: US/11/036,317
; CURRENT PRILICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                Gaps
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US-10-719-900-599645

Sequence 599645, Application US/10719900

Publication No. US20050026164A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

PRIOR PILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60427,808

PRIOR FILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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                                                3; Indels
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78.3%; Pred. No. 5.4e+03;
iive 0; Mismatches 5;
Query Match 63.3%; Score 15.2; DB 9; Best Local Similarity 85.0%; Pred. No. 4.4e+03; Matches 17; Conservative 0; Mismatches 3;
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US-10-809-189-57613/c
Sequence 57613, Application US/10809189
; Publication No. US20050048531A1
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Best Local Similarity 85.03
Matches 17; Conservative
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Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
CORGANISM: Mus musculus
US-11-036-317-523845
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; Sequence 692355, Application No. US20040146910A1
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICATT: Xue Mei Zhou
; TITLE OP INVENTION:
; TITLE OP INVENTION: WHERE: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; FRIOR PAPLICATION NUMBER: 60/427,836
; FRIOR FILING DATE: 2002-11 20
; NUMBER OF SEQ ID NOS: 699466
; SOPTWARE: Microarray Probe Sequence Listing Generator V 1.1
; TENCH CONTROL OF SEQUENCE CONTROL OF SEQUENCE LISTING GENERATOR OF SEQ ID NOS: 699466
; SEQ ID NO 692355
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US-10-719-900-648791/c

Sequence 648791, Application US/10719900

Sequence 648791, Application US/10719900

GENERAL INFORMATION:

TITLE OF INVENTION: Methods of Genetic Analysis of Mouse:

TITLE OF INVENTION: Methods of Genetic Analysis of Mouse:

TITLE OF INVENTION: WHENCE: 3528.1

CURRENT APPLICATION NUMBER: 05/10/719,900

CURRENT FILING DATE: 2003-11-20

PRIOR FILING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 61.7%; Score 14.8; DB 7; Length 25; Best Local Similarity 88.9%; Pred. No. 6.7e+03; Matches 16; Conservative 0; Mismatches 2; Indels
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88.9%; Pred. No. 6.7e+03;
ive 0; Mismatches 2; Indels
                                                                                                                                        Length 25;
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                                                                                                                                   Score 14.8; DB 7;
Pred. No. 6.7e+03;
0; Mismatches 2;
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                                                                                                                                        Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                       6 ACAGCTGGGGAACAAGAC
                                               ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-2771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Rattus norvegicus
US-10-719-956-692355
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Best Local Similarity 88.9
Matches 16; Conservative
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CORGANISM: Mus musculus
US-10-719-900-648791
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; SEQ ID NO 2771
                        LENGTH:
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Publication No. US20050118625A1

GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Weath
APPLICANT: Wounts, William
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT PILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 14605
LENGTH: 25
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; Bellication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Value Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; PLE REPERRENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR APPLICATION NUMBER: 60/427,836
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15; DB 9; Lengtn 23, Pred. No. 5.48+03;
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              APPLICANT: Michael Mittmann
APPLICANT: Machael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Afgrmetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/10/809,189
CURRENT PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: US/09/396,196
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: PASTERO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 62.5%; Score 15; DB Best Local Similarity 78.3%; Pred. No. 5.4e Matches 18; Conservative 0; Mismatches
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; ORGANISM: Probe Sequence
US-10-956-157-14605
                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: mus musculus
US-10-809-189-57613
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US-10-719-900-58299/c
Sequence 5829, Application US/10719900
; Sequence 5829, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse; FILE REFERENCE: 3520: I
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR PILING DATE: 2003-11-20
; PRIOR FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SEQ ID NO 58299
; LENGTH: 25
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Sequence 198954, Application US/10719956

Publication No. US20040146910A1

GENERAL INFORMATION:
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1

CURRENT APPLICATION NUMBER: US/10/719,956

CURRENT PILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,836

PRIOR RELING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 699466

SOFTWARE MICROARRAY Probe Sequence Listing Generator V 1.1

SEQ ID NO 198954

LENGTH: 25
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Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4;
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81.0%; Pred. No. 8.3e+03;
tive 0; Mismatches 4;
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60.8%; Score 14.6; DB 8;
Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4;
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; ORGANISM: Rattus norvegicus
US-10-719-956-198954
                                              TYPE: DNA
CRGANISM: Rattus norvegicus
US-10-719-956-198953
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US-10-719-900-58299
SEQ ID NO 198953
LENGTH: 25
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                                 Sequence 115950, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
HUMAN WEEL
TITLE OF INVENTION: HUMAN OSTECARTHRITIS AND HUMAN PROTEASES
TITLE OF INVENTION: HUMAN OSTECARTHRITIS AND HUMAN PROTEASES
TITLE OF INVENTION: HUMAN OSTECARTHRITIS AND HUMAN PROTEASES
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 315950
LENGTH: 25
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Sequence 436639, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

TITLE OF INFURINCE: Method of Analysis of Alternative Splicing in Mouse

FILE REPERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR APPLICATION NUMBER: US 60/536,639

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25

LENGTH: 25
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; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: YUE Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR APPLICATION NUMBER: 60/427,836
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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CORGANISM: Mus musculus
US-11-036-317-436639
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Sequence 14666, Application US/10956157

Sequence 14666, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Worth

APPLICANT: Worth

TITLE OF INVENTION: HUMAN OSTBOARTHRITIS AND HUMAN PROTEASES

TITLE OF INVENTION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: PatentIn version 3.2

LENGTH: 25
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US-11-036-317-81764

Sequence 817-64, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

APPLICANT: Blume, John

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REPERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT PILING DATE: 2005-01-13

PRIOR PILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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                                                                                                                        Length 25;
                                                                                                                     Score 14.6; DB 9;
Pred. No. 8.3e+03;
0; Mismatches 4;
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                                                                                                                        Query Match
Best Local Similarity 81.0%;
Matches 17; Conservative
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Best Local Similarity 81.0°
Matches 17; Conservative
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; ORGANISM: Probe Sequence
US-10-956-157-14606
                        TYPE: DNA
CORGANISM: Probe Sequence
US-10-956-157-14604
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US-11-036-317-81764
LENGTH: 25
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TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REPERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PALENTIN VERSION 3.2
SEQ ID NO 14604
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; Sequence 267622, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse;
FILE REFERENCE: 3528.1
; CURRENT PAPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR APPLICATION NUMBER: 60/427,808
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 267622
; LENGTH: 25
                                        Sequence 267621, Application US/10719900
| Publication No. US20050026164A1
| GENERAL INFORMATION:
| APPLICANT: Xue Mei Zhou
| TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
| TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
| TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
| TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
| CURRENT APPLICATION NUMBER: 60/427,808
| PRIOR PELING DATE: 2003-11-20
| NUMBER OF SEQ ID NOS: 982914
| SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
| LENGTH: 25
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60.8%; Score 14.6; DB 8;
Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4;
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Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
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US-10-719-900-267621
                          -10-719-900-267621/c
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US-11-036-317-552223
i Sequence 552223, Application US/11036317
i Publication No. US20060214823A1
i GENERAL INFORMATION:
i APPLICANT: Williams, Alan
i APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
i FILE REFERENCE: 3654.1
i CURRENT APPLICATION NUMBER: US/11/036,317
i CURRENT PILING DATE: 2005-01-13
i PRIOR PILING DATE: 2004-01-13
i NUMBER OF SEQ ID NOS: 991174
i SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
i SEQ ID NO 552223
LENGTH: 25
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| Sequence 770140, Application US/11036317 |
| Publication No. US20050214823A1 |
| Publication No. US20050214823A1 |
| GENERAL INFORMATION: |
| APPLICANT: Williams, Alan |
| APPLICANT: Williams, John |
| TILLE OF INVENTION: Wethod of Analysis of Alternative Splicing in Mouse |
| FILE REPERENCE: 3654.1 |
| CURRENT APPLICATION NUMBER: US/11/036,317 |
| CURRENT FILING DATE: 2005-01-13 |
| PRIOR APPLICATION NUMBER: US 60/536,639 |
| PRIOR FILING DATE: 2004-01-13 |
| PRIOR FILING DATE: 2004-
US-11-036-317-189892/c
; Sequence 189892, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
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CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 189892

LENGTH: 25
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Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ATGCACAGCTGGGGAACAAGA 22
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CORGANISM: Mus musculus
US-11-036-317-189892
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US-11-036-317-552223
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Sequence 1997, Application US/10349143

Sequence 1997, Application No. US20040005584A1

Publication No. US20040005584A1

GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
SAPPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/10/349,143

CURRENT FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US 60/109,732
PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-23
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796
SEQ ID NOS: 11796
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j Sequence 520335. Application US/10719900

j Publication No. US20050026164A1

GENERAL INFORMATION:

j APPLICANT: Xue Mei Zhou

j TITLE OF INVENTION: Methods of Genetic Analysis of Mouse;

FILE REFERENCE: 3528.1

CURRENT FILING DATE: 2003-11-20

PRIOR PRIOR PAPLICATION NUMBER: 60/427,808

PRIOR FILING DATE: 2002 11 20

j RNDMARE: Microarray Probe Sequence Listing Generator V 1.1

j SORTWARE: Microarray Probe Sequence Listing Generator V 1.1

j SEQ ID NO 520335
                                                                                                                                                                                                               Length 25;
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NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 770140
LENGTH: 25
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LOCATION: 24
CTHER INFORMATION: 99-7877-363 : polymorphic base A or G
US-10-349-143-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 60.8%; Score 14.6; DB 6; 1
Best Local Similarity 73.9%; Pred. No. 8.2e+03;
Matches 17; Conservative 1; Mismatches 5;
                                                                                                                                                                                                               60.8%; Score 14.6; DB 10;
81.0%; Pred. No. 8.3e+03;
tive 0; Mismatches 4;
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                                                                                                                                                                                                                                                                     17; Conservative
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ORGANISM: Homo Sapiens
                                                                                                                   TYPE: DNA
CORGANISM: Mus musculus
US-11-036-317-770140
                                                                                                                                                                                                                                    Best Local Similarity
Matches 17; Conserv
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US-10-349-143-1997
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US-11-036-317-183105/c
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Sequence 46464, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT PILING DATE: 2005-01-13

PRIOR PILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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                                                                                                                                                                                                                                                                                Sequence 520337, Application US/10719900
; Sequence 520337, Application US/10719900
; Publication No. US2005026164A1
; GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REPERENCE: 3528.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 05/10/719,900
; PRIOR FILING DATE: 2003-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 520337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 60.0%; Score 14.4; DB 10; Length 25; Best Local Similarity 93.8%; Pred. No. 1e+04; Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.0%; Score 14.4; DB 8; Length 25; 75.0%; Pred. No. 1e+04; tive 0; Mismatches 6; Indels
                                                                                  Query Match 60.0%; Score 14.4; DB 8; Length 25; Best Local Similarity 75.0%; Pred. No. 1e+04; Matches 18; Conservative 0; Mismatches 6; Indels
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---- 6; Indels
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Matches 18; Conservative
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                      ) ORGANISM: Mus musculus
US-10-719-900-520335
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  TYPE: DNA
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RESULT 39

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Sequence 271344, Application US/11036317
; Sequence 271344, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION: NUMBER: US/11/036,317
; CURRENT PILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 271344
; Sequence 183105, Application US/11036317; Sequence 183105, Application No. US20050214823A1; Publication No. US20050214823A1; GENERAL INFORMATION:
; APPLICANT: Williams, Alan; APPLICANT: Blume, John; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse; FILE REFERENCE: 3654.1
; CURRENT FILING DATE: 2005-01-13; PRIOR APPLICATION NUMBER: US 60/536,639; PRIOR FILING DATE: 2004-01-13; NUMBER OF SEQ ID NOS: 991174; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SRO ID NO 183105
; LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 25;
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Best Local Similarity 93.8
Matches 15; Conservative
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; ORGANISM: Mus musculus
US-11-036-317-271344
                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-183105
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Matches 15; Conserve
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CENGTH:
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Sequence 7086, Ap
Sequence 12144, A
Sequence 1898, Ap
Sequence 6784, Ap
Sequence 6784, Ap
Sequence 8469, Ap
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Sequence 57613, A
Sequence 11, Appl
Sequence 1997, Ap
Sequence 103166,
Sequence 6696, Ap
                                                                                                                               December 13, 2005, 13:14:34 ; Search time 104.5 Seconds (without alignments) 408.244 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/5_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/P_CTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/P_COMB.seq:*
/cgn2_6/ptodata/1/ina/P_COMB.seq:*
/cgn2_6/ptodata/1/ina/P_COMB.seq:*
/cgn2_6/ptodata/1/ina/PE_COMB.seq:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-537-811-13

US-09-422-978-1997

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US-10-131-827-6996

US-10-131-827-7086

US-09-422-978-1898

US-09-422-978-1898

US-10-131-827-6784

US-10-131-827-6784

US-10-131-827-6784

US-10-131-827-6784

US-09-866-108A-13362

US-09-866-108A-13362

US-09-866-108A-13365

US-09-866-108A-13369

US-09-422-978-3886-108A-13369

US-09-422-978-3886-108A-13369

US-09-422-978-3886-108A-13369

US-09-422-978-3886-108A-13369
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                                                                                                                                                                                                                                                                                                                                                 1303057 seqs, 888780828 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                               - nucleic search, using sw model
                                                                                                                                                                                                                                                                                       IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Issued Patents NA:*
                                                                                                                                                                                                           US-10-713-137-3
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US-09-101-927-5
US-08-679-645-361
US-09-644-859-6
US-09-220-557-11
US-09-220-557-11
US-09-396-1964-8421
US-09-396-1964-8421
US-09-396-1964-86727
US-09-396-1964-8727
US-09-033-428-18
US-09-614-495-17
US-09-898-883-18
US-09-897-259C-6
US-09-897-259C-6
US-09-897-259C-6
US-09-897-259C-6
US-09-814-292-38
US-09-897-259C-6
US-09-897-259C-6
US-09-814-292-38
US-09-897-259C-6
US-09-814-292-38
US-09-817-259C-6
US-09-817-259C-6
US-09-817-259C-6
US-09-817-292-38
US-09-817-259C-6
US-09-817-292-38
US-09-817-292-38
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Patent No. 6821724;
GENERAL INFORMATION:
APPLICANT: Michael Mittmann;
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: Affymetrix, Inc.;
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT FILING DATE: 1999-09-15
PRIOR PILICATION NUMBER: 60/100,678
PRIOR PILICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOUTWARE: PRESEEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                      US-09-396-196G-14507
US-09-396-196G-22239
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Best Local Similarity 85.0
Matches 17; Conservative
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CORGANISM: mus musculus
US-09-396-196G-92895
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Best Local Similarity 78.3%; Pred. No. 1.2e+03; Matches 18; Conservative 0; Mismatches 5; Indels
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ORGANISM: Homo Sapiens
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US-09-422-978-1997
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APPLICANT: CHO, DEOG YOUNG
APPLICANT: KIM, CHON HYUNG
APPLICANT: KIM, CHON HYUNG
APPLICANT: YANG, JAE YOUNG
APPLICANT: YANG, JAE YOUNG
APPLICANT: YANG, JAE YOUNG
APPLICANT: YANG, JAE YOUNG
APPLICANT: XIM, JOO HO
TITLE OF INVENTION: IMPROVED HCV DIAGNOSTIC
TITLE OF INVENTION: AGENTS
NUMBER OF SEQUENCES: 48
CONTRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 AVENUE OF the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER: TEADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: SEALSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,811
FILING DATE: 24-OCT-1995
CLASSIFICATION NUMBER: PCT/KR94/00040
FILING DATE: 29-APP-1993
ATTORNEY/AGENT: NUMBER: KR 93-7440
FILING DATE: 39-APR-1993
ATTORNEY/AGENT: NUMBER: KR 93-7440
APPLICATION NUMBER: KR 93-7440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Jones, III, Harry C
REGISTRATION NUMBER: 20,280
REGISTRATION NUMBER: 20,280
REFERENCE/DOCKET NUMBER: 8512-037-999
TELEPHONE: 212-790-9090
TELEPAX: 212-69-9741
TELEPAX: 66141 PENNIE
INFORMATION POR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDENNESS: single
     NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 57613
LENGTH: 25
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US-08-537-811-13
                                                                                                                                                                                                                                                                                                                     2 ATGCACAGCTGGGGAACAAGACG 24
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Patent No. 5910405
GENERAL INFORMATION:
                                                                                                             ; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-57613
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DB 2; Length 38;

62.5%; Score 15;

Query Match

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Sequence 1997, Application US/09422978
; Sequence 1997, Application US/09422978
; Sequence 1997, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Chumenfed, Marta
; APPLICANT: Chumenfed, Marta
; APPLICANT: Chumenfed, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...;
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...;
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...;
; TAPLICANT: 1999-10-20
; EARLIER FILING DATE: 1999-10-20
; EARLIER FILING DATE: 1999-04-21
; EARLIER FILING DATE: 1998-11-23
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; TUMENGE OF SEQ ID NOS: 11796
; TUMENGER OF SEQ ID NOS: 11796
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US-09-422-978-1997
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US-09-396-103166
i Sequence 103166. Application US/09396196G
j Patent No. 6821724
j GENERAL INFORMATION:
APPLICANT: Michael Mittmann
j APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: AFF/MELTIX, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: 60/100,678
FILE REPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SEQ ID NO 103166
LENGTH: 25
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
60.8%; Score 14.6; DB 3;
Best Local Similarity 73.9%; Pred. No. 1.8e+03;
Matches 17; Conservative 1; Mismatches 5;
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35 gergakckécrégéakáckeke 13
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CORGANISM: mus musculus
US-09-396-196G-103166
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58.3%; Score 14; DB 3; Length 47;

Best Local Similarity 87.5%; Pred. No. 3.5e+03;

Matches 14; Conservative 1; Mismatches 1; Indels
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58.3%; Score 14; DB 3; Length 25;
Best Local Similarity 77.3%; Pred. No. 3.2e+03;
Matches 17; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-718-261 : polymorphic base A or
US-09-422-978-1898
                                                      Sequence 32344, Application US/09396196G
; Sequence 32244, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: David Mack
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 TGCACAGCTGGGGAACAAGACG 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-396-196G-32344
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US-09-422-978-1898
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Sequence 7086, Application US/10131827

Batent No. 6905827

GENERAL INFORMATION:

APPLICANT: Woolgemuth, Jay

TITLE OF INVENTION: UNSCRIPTION: CHRONIC INFLAMMATORY DISEASES

TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES

FILE REFERENCE: 506612000120

CURRENT FILING DATE: 2002-09-06

PRIOR PLILOR DATE: 2001-06-08

PRIOR PPLICATION NUMBER: US 60/296,764

PRIOR PLILOR DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 9090

SOFTWARE: PatentIn version 3.1

SEQ ID NO 7086

LENGTH: 50
                                                                                                                                   Sequence 66956, Application US/10131827

Sequence 66956, Application US/10131827

Sequence 66956, Application US/10131827

GENERAL INFORMATION:
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Ly, NGOC
ITILE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
ITILE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
ITILE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
ITILE OF INVENTION: MUMBER: US/10/131,827

CURRENT PILING DATE: 2001-09-06

PRIOR APPLICATION NUMBER: US 60/296,764

SEQ ID NOS: 9090

SEQ ID NOS: 9090

SEQ ID NOS: 9096

LENGTH: 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 14.2; DB 3; Length 50;
Pred. No. 2.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
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5 CACAGCTGGGGAACAAGAC 23
                                        5 CATGGCTGTGGAACAAGAC 23
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Best Local Similarity 84.2%;
Matches 16; Conservative (
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA; ORGANISM: Homo sapiens
US-10-131-827-7086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens US-10-131-827-6696
                                                                                                                              US-10-131-827-6696
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APPLICANT: SHANNOW, Mark

TITLE OF INVENTION: WAYSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR PEDLICATION NUMBER: US 60/207,456
PRIOR PEDLICATION NUMBER: US 60/207,456
PRIOR PELLING DATE: 2000-09-26
PRIOR PELLING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PELLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PELLING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
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patent No. 628463

general No. 628463

general Information:

APPLICANT: Hasebe, Masahisa

APPLICANT: Tosu, Mariko

TILE OF INVENTION: Method for Detection of Mutations
FILE REFERENCE: PU96-1684

CURRENT PELLING DATE: 1999-08-18

PRIOR FILING DATE: 1999-08-18

PRIOR PELLING DATE: 1997-08-29

PRIOR PLING DATE: 1996-06-29

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 5: 12

LENGTH: 20
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ORGANISM: synthetic construct
                                                                   PENN, Sharron G.
HANZEL, David K.
RANK, David R.
CHEN, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.2°
...heg 15; Conservative
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US-10-131-84.7-6394
Sequence 6394, Application US/10131827
Fatent No. 6905827
GENERAL INFORMATION:
APPLICANT: Wohlgemuth, Jay
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
TITLE OF INVENTION: MUNBER: US/10/131,827
CURRENT FILING DATE: 2000-09-06
PRIOR FILING DATE: 2001-06-08
PRIOR PLILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-06-08
SEQ ID NOS: 9090
SEQ ID NO 6394
LENGTH: 50
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APPLICANT: Wohlgemuth, Jay
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: CRRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 566612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT PILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 58.3%; Score 14; DB 3; Length 50; Best Local Similarity 100.0%; Pred. No. 3.5e+03; Matches 14; Conservative 0; Mismatches 0; Indels
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Sequence 8469, Application US/09866108A
Patent No. 6686188
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Patent No. 6905827
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Best Local Similarity 100.
Matches 14; Conservative
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CORGANISM: Homo sapiens
US-10-131-827-6784
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LENGTH: 50
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APPLICANT: CHEN, WEARDERS
APPLICANT: SHANNOW, MARK
TITLE OF INVENTION: MYGIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEADWICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT PILING DATE: 2001-05-25
FRIOR APPLICATION NUMBER: US 60/207,456
FRIOR PILING DATE: 2000-05-26
FRIOR PILING DATE: 2000-05-26
FRIOR PLING DATE: 2000-05-26
FRIOR PLING DATE: 2000-09-27
FRIOR PLING DATE: 2000-09-27
FRIOR APPLICATION NUMBER: US 60/236,359
FRIOR PLING DATE: 2000-09-27
FRIOR PLING DATE: 2000-09-27
FRIOR PLING DATE: 2001-01-30
FRIOR FILING DATE: 2001-01-30
FRIOR FILING DATE: 2001-01-30
FRIOR FILING DATE: 2001-01-30
FRIOR FILING DATE: 2001-01-30
FRIOR PLING DATE: 2001-01-30
FRIOR FILING DATE: 2001
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i Sequence 13363, Application US/09866108A

j Patent No. 6686108

general incordation:
    APPLICANT: GU, Yizhong

j APPLICANT: GU, Yizhong

APPLICANT: HANZEL, David K.

APPLICANT: HANZEL, David K.

APPLICANT: HANZEL, David K.

APPLICANT: HANZEL, David K.

APPLICANT: HANZEL, David R.

APPLICANT: HANZEL, David R.

APPLICANT: HANZEL, David R.

APPLICANT: SHANNON, Mark

ITILE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: AEOMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108A

CURRENT PILING DATE: 2000-05-25

PRIOR FILING DATE: 2000-10-36

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-06

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2001-130

PRIOR FILING DATE: 2001-130

PRIOR FILING DATE: 2001-130

PRIOR FILING DATE: 2001-130

PRIOR FILING DATE: 2001-130
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Best Local Similarity 88.2
Matches 15; Conservative
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APPLICANT: HANZEL, David K.
APPLICANT: RANK, David K.
APPLICANT: RANK, David R.
APPLICANT: RENK, David R.
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE FILE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE CURRENT APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-00-06
PRIOR PLILING DATE: 2000-10-04
PRIOR PLILING DATE: 2000-10-04
PRIOR PLILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PLILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR PRILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR PRILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR PRILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PRILING PAPEL CATION NUMBER: PCT/US01/00668
PRIOR PRILING PAPEL CATION NUMBER: PCT/US01/00668
PRIOR PRILING PAPEL CATION DATE: PCT/US01/00668
PRIOR PRILING PAPEL CATION DATE: PCT/US01/00668
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PRIOR PRILING PAPEL CATION DATE PUBLICATION DAT
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                                                                         57.5%; Score 13.8; DB 3; Length 20; 88.2%; Pred. No. 3.9e+03; ive 0; Mismatches 2; Indels
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Patent No. 6686188
SEQ ID NO 13361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-866-108A-13361
; Sequence 13361, Application US/09866108A
; Patent No. 6686188
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                                                                                                                                                                                                                                                 6 ACAGCTGGGGAACAAGA 22
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APPLICANT: GU, Yizhong
APPLICANT: GI, Yongang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David K.
APPLICANT: CHEN, Wensheng
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Best Local Similarity 88.2<sup>3</sup>
Matches 15; Conservative
                                                                                                                                                                   Conservative
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                                                                             Query Match
Best Local Similarity
Matches 15; Conserv
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US-09-194-478-5
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; ORGANISM: Homo sapiens
US-09-866-108A-13364
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US-09-866-108A-13365
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Sequence 13364, Application US/0986610BA
Sequence 13364, Application US/0986610BA
GENERAL INCRAMATION:
APPLICANT: GU, Yizhong
APPLICANT: PENN, Sharron G.
APPLICANT: RANK, David K.
APPLICANT: RANK, Banaheng
APPLICANT: RANK, Banaheng
APPLICANT: RANK, Mensheng
APPLICANT: ALMON, MALK
ITILE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUWAN HEART AND MUSCLE
TILE REFERENCE: AEOMICA-7
CURRENT FILING DATE: 2001-05-25
PRIOR PELLOATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-06-36
PRIOR PILING DATE: 2001-00-4
PRIOR PELLOATION NUMBER: DCT/USO1/00666
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR PILING DATE: 2001-01-30
PRIOR PELLOATION NUMBER: PCT/USO1/00669
PRIOR PILING DATE: 2001-01-30
PRIOR
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PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR DATE: 2001-01-30
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Best Local Similarity 88.2%;
Matches 15; Conservative
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CORGANISM: Homo sapiens
US-09-866-108A-13363
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US-99 E66-10MA-11365, Application US/09866108A

Patent No. 666618B

Saguence 13365, Application US/09866108A

Patent No. 666618B

SAPLICANT: GU, Yizhong

APPLICANT: GU, Yizhong

APPLICANT: HANZEL, David K.

APPLICANT: HANZEL, David R.

CURRENT APPLICATION WORBER: US 60/207,456

PRIOR PILING DATE: 2000-09-26

PRIOR PILING DATE: 2000-09-26

PRIOR PILING DATE: 2001-01-30

PRIOR PELING DATE: 2
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        ; DB 3; Length 25;
4e+03;
                                                                                     Indels
Query Match
57.5%; Score 13.8; I
Best Local Similarity 88.2%; Pred. No. 4e+C
Matches 15; Conservative 0; Mismatches
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; Sequence 13366, Application US/09866108A
; Parent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
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APPLICANT: RANK, David R.

APPLICANT: RANK, David R.

APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON: MAK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-10-04
PRIOR PLILING DATE: 2000-09-27
PRIOR PLILING DATE: 2001-00-27
PRIOR PLILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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PRIOR PELING DATE: 2
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 15; Conserv
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US-09-866-108A-13368
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                                                                                        APPLICANT: HANKLEL, David R.
APPLICANT: HANKLEL, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
TITLE OF INTERIOR HANCEL, David Mark
TITLE OF INTERIOR: AECMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/206,359
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
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APPLICANT: PENN, Sharron G.
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: SHANNON, MARK
APPLICANT: SHANNON, MARK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-06-67
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-09-27
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NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Acomica Sequence Listing Engine
Patent No. 6866188
SEQ ID NO 13366
LENGTH: 25
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-hes 2; Indels
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Pred. No. 4e+03;
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US-09-866-108A-13367
; Sequence 13367, Application US/09866108A
; Patent No. 6686188
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Best Local Similarity 88.2%;
Matches 15; Conservative (
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-866-108A-13366
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RESULT 25
US-09-101-927-5
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US.09-866-108A-13569
US.09-866-108A-13569
Patent No. 6666189
GERERAL INCORMATION:
APPLICANT: J. Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: PENN, Sharron G.
APPLICANT: AMERICAN G.
APPLICANTON INVERS: 2001-06-25
FRIOR APPLICATION NUMBER: US 60/207,456
FRIOR APPLICATION NUMBER: US 60/207,456
FRIOR APPLICATION NUMBER: US 60/206,556
FRIOR APPLICATION NUMBER: US 60/206,566
FRIOR APPLICATION NUMBER: PCT/US01/0066
FRIOR PRING DATE: 2001-01-30
FRIOR PLING DATE: 2001-01-30
FRIOR PLING DATE: 2001-01-30
FRIOR PLING DATE: 2001-01-30
FRIOR APPLICATION NUMBER: PCT/US01/0066
FRIOR APPLICATION NUMBER: PCT/US01/0066
FRIOR APPLICATION NUMBER: PCT/US01/0066
FRIOR PLING DATE: 2001-01-30
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                                                                                                         Score 13.8; DB 3; Length 25;
Pred. No. 4e+03;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeemica Sequence Listing Engine Patent No. 6686188
SEQ ID NO 13369
LENGTH: 25
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                                                                                                                                                                                                                                                                     2 AGCTGGAGAACATGACG 18
                                                                                                                                                                                                                                 8 AGCTGGGGAACAAGACG 24
                                                                                                               Query Match 57.5%;
Best Local Similarity 88.2%;
Matches 15; Conservative (
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CORGANISM: Homo sapiens
US-09-866-108A-13369
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13368
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Sequence 3853, Application US/09422978 Patent No. 6537751 GENERAL INFORMATION:

US-09-422-978-3853/c

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APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, 11ya
TITLE OF INTENTION: Biallic markers for use in constructing a high density...
FILE STEERENCE: GENSET.020CP1
CURRENT PILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER PILING DATE: 1999-04-21
EARLIER PELING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER REPLING DATE: 1998-11-23
EARLIER PILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-26
EARLIER PILING DATE: 1998-11-27
EARLIER FILING DATE: 1998-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 57614, Application US/09396196G
; Sequence 57614, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION.
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE NEFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR REPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOSTWARE: FREESEQ for Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.7%; Score 13.6; DB 3;
80.0%; Pred. No. 4.9e+03;
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Pred. No. 4.3e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ATGCACAGCTGGGAACAAG 21
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Best Local Similarity 78.99
Matches 15; Conservative
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Best Local Similarity 80.0
Matches 16; Conservative
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US-09-396-196G-57614
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo Sapiens
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US-09-396-196G-57614/C
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LOCATION: 24
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LENGTH: 25
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us-10-713-137-3.sizlim.rni

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US-09-64-4858-6

US-09-644-858-6

Sequence 6, Application US/09644858

Patent No. 6933364

GENERAL INFORMATION:

APPLICANT: Tosho Corporation

APPLICANT: Hattori, Yoshiyuki

APPLICANT: Hattori, Yoshiyuki

APPLICANT: Hattori, Yoshiyuki

TITLE OF INVENTION: SECRETORY THYROID STIMULATING HORMONE RECEPTOR, AND METHOD FOR

TITLE OF INVENTION: ANTI-THYROID STIMULATING HORMONE RECEPTOR ANTIBODY USING THE SI

FILE REFERENCE: PA21-046

CURRENT APPLICANION NUMBER: US/09/644,858

CURRENT FILING DATE: 2000-08-24

NUMBER OF SEQ ID NOS: 25

SOSTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.7%; Score 13.6; DB 3; Length 49;
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Batent No. 6515206

GENERAL INFORMATION:
APPLICANT: Chaudhuri, Sumita
TITLE OF INVENTION: PLASTID TRANSFORMATION OF BRASSICA
TITLE REPRENCE: 15398/00/US
CURRENT APPLICATION NUMBER: US/09/220,557A
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 11
LENGTH: 49
                                                                                                                                          ; OTHER INFORMATION: The letter "N" stands for any base. US-08-679-645-361
                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                            Score 13.6; DB 3;
Pred. No. 5.1e+03;
2; Mismatches 5;
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; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-220-557-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature; LOCATION: ()...(); COTHER INFORMATION: sense primer shTSHR-205-044-858-6
                                                                                                                                                                                                                                                                                                                                    1 GATGCACAGCTGGGGAACAAG 21
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                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial/Unknown
                          LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLCY: linear
FEATURE:
  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 28
US-09-220-557-11/c
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LENGTH: 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zwick, Michael G.
APPLICANT: Zwick, Michael G.
APPLICANT: Zwick, Michael G.
APPLICANT: Edington, Brent E.
APPLICANT: McSwiggen, James A.
APPLICANT: Merlo, Patricia Ann Owens
APPLICANT: Skokut, Thomas A.
APPLICANT: Skokut, Thomas A.
APPLICANT: Skokut, Thomas A.
APPLICANT: Scott A.
APPLICANT: Folkerts, Otto
APPLICANT: Folkerts, Otto
APPLICANT: Merlo, Donald J.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR
TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
TITLE OF INVENTION: IN PLANTS
NUMBER OF SEQUENCES: 1263
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Sailte 4700
CURRENT APPLICATION NUMBER: US/09/101,927
CURRENT FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: PCT/US97/026735
EARLIER APPLICATION NUMBER: 60/012,218
EARLIER APPLICATION NUMBER: 60/012,218
EARLIER APPLICATION NUMBER: 60/012,218
EARLIER FILING DATE: 1996-02-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/679,645
FILING DATE: J1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 06/001,135
FILING DATE: J1995
APPLICATION NUMBER: 08/300,726
APPLICATION NUMBER: 08/300,726
APPLICATION NUMBER: 08/300,726
ATTORNEY,AGENT INFORMATION:
NAME: WARDLEY, RICHARD J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
RELECHONE: (213) 489,1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: SIS Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 361, Application US/08679645
Patent No. 6350934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GATGCACAGCTGGGGAACAA 20
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INFORMATION FOR SEQ ID NO: 361:
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                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-101-927-5
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Sequence 107466, Application US/09396196G

Patent No. 6821724

GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: AFFWENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
FILE REFERENCE: 3101.1
CURRENT FILING DATE: 1999-09-15
PRIOR PLING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 107466
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 13.4; DB 3;
Pred. No. 6.1e+03;
                                             Sequence 95727, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affamerix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/396,196G CURRENT FILING DATE: 1999-09-15 PRIOR PPLICATION NUMBER: 60/100,678 PRIOR FILING DATE: 1998-09-17 NUMBER OF SEQ ID NOS: 127806 SOFFWARE: FascSEQ for Windows Version 4.0 SEQ ID NO 95727
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Patent No. 6197293;
GENERAL INFORMATION:
APPLICANT: Yu, De Chao
APPLICANT: Schuur, Eric
APPLICANT: Henderson, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 TGCACAGCTGGGGAA 17
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Best Local Similarity 73.3.
Best Local 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: mus musculus US-09-396-196G-107466
                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: mus musculus
US-09-396-196G-95727
                                       US-09-396-196G-95727
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                     Gaps
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Pred. No. 6.1e+03;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 49;
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                     Indels
                                                                                                                                                                                            Sequence 11, Application US/10219227

Patent No. 6891086

GENERAL INFORMATION:
APPLICANT: Oakes, Janette V.
APPLICANT: Oaken, Janette V.
TILE OF INVENTION: PLASTID TRANSFORMATION OF BRASSICA
FILE REFERENCE: 15398/01/US
CURRENT FILING DATE: 2002-08-15
PRIOR FILING DATE: 1999-12-17
PRIOR PLICATION NUMBER: US/09/465,856
PRIOR PLICATION NUMBER: US/09/465,856
PRIOR PLICATION NUMBER: US/09/465,856
PRIOR APPLICATION NUMBER: 09/220,557
PRIOR PLING DATE: 1999-12-17
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-396-196G-88421
; Sequence 88421. Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
APPLICANT: Michael Mittmann
; APPLICANT: David Mack
APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FRSESQ for Windows Version 4.0
; SEQ ID NO 88421
80.0%; Pred. No. 5.4e+03; tive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.0%; Pred. No. 5.4e+03;
Matches 16; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
FRATURE:
CTHER INCRMATION: Synthetic Oligonucleotide
US-10-219-227-11
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                                                              S CACAGCTGGGGAACAAGACG 24
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Best Local Similarity 73.9%;
Matches 17; Conservative
Best Local Similarity 80.0 Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: mus musculus
US-09-396-196G-88421
                                                                                                                                                                  RESULT 29
US-10-219-227-11/c
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Gaps ö

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GENERAL INFORMATION:
APPLICANT: Henderson, Daniel R.
APPLICANT: Henderson, Daniel R.
APPLICANT: Yu, De Chao
TITLE OF INVENTION: HETEROLOGOUS TRANSCRIPTION REGULATORY ELEMENTS AND
TITLE OF INVENTION: HETEROLOGOUS TRANSCRIPTION REGULATORY ELEMENTS AND
TITLE OF INVENTION: HETEROLOGOUS TRANSCRIPTION REGULATORY ELEMENTS AND
TITLE OF INVENTION: OF USING SAME
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 75S PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
COUNTRY: LBA COMPALIA
COMPUTER: LBA COMPALIA
COMPUTER: LBA COMPALIA
COMPUTER: BASTEM: Windows
SOFTWARE: FastSE for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/033,556
FILING DATE:
FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.8%; Score 13.4; DB 3; Length 30; 73.9%; Pred. No. 6.3e+03; ive 0; Mismatches 6; Indel8
                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: POLIZI, CATHERIUE M.
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 34802-30004.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-560
TELEFAX: (415) 494-0792
IPORRATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
            APPLICATION NUMBER: US/09/033,428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ATGCACAGCTGGGGAACAAGACG 24
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Patent No. 6432700
GENERAL INFORMATION:
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TELEX: 70641
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 30 base palrs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 55.8
Best Local Similarity 73.9
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                 FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-033-556-40/c
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US-09-033-556-40
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            ADENOVIRUS VECTORS SPECIFIC
FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS OF USE
THEREOF
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Sequence 18, Application US/09033428

Sequence 18, Application US/09033428

Sequence 18, Application US/09033428

Patent No. 6254862

GENERAL INFORMATION:
APPLICANT: Little, Andrew
APPLICANT: Little, Andrew
APPLICANT: Henderson, Daniel
TITLE OF INVENTION: EXPRESSING APHA-FETOPROTEIN AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 23
CORRESPONDENCES: MORISON & FOERSTER
STREET: 755 PAGE MILL ROAD

CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 55.8%; Score 13.4; DB 3; Length 3 Best Local Similarity 73.9%; Pred. No. 6.3e+03; Matches 17; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC TITLE OF INVENTION: FOR CELLS EXPRESSING ANDROGE TITLE OF INVENTION: FOR CELLS EXPRESSING ANDROGE NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS: 22 CORRESPONDENCE ADDRESS: 4DRESSE: 4DRESSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELBEAX: 650
TELER: 706141
INFORMATION FOR SEQ ID NO: 17
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
""DR: mucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , TOPOLOGY: linear
US-09-033-333-17
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Schuur, Eric
Henderson, Daniel
TITLE OF INVENTION: EXPRESSING APHA-FETOPROTEIN AND METHODS OF USE THEREOF
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Best Local Similarity 73.9%; Pred. No. 6.3e+03;
Matches 17; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                         COUNTY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DAY SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,883
FILING DATE: 02-Jul-2001
CLASSIFICATION NUMBER: US/09/033,428
APPLICATION NUMBER: US/09/033,428
FILING DATE: CUNKNOWN:
NAME: POLIZI, CATHERINE M.
NAME: POLIZI, CATHERINE M.
NAME: POLIZI, CATHERINE M.
REGERENTION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 34802-30004.00
TELEPPANE: (415) 494-0792
TELEPPANE: (415) 494-0792
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US-08-462-159B-6/c
| Sequence 6, Application US/08462159B
| Patent No. 6787640
| GENERAL INFORMATION:
| APPLICANT: Greene Ph.D., John M.
| APPLICANT: Dillon Ph.D., Patrick J.
| TILLE OF INVENTION: Fibroblast Growth Factor 14
| NUMBER OF SEQUENCES:
| ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
| ADDRESSEE: Stewart & Olstein
| STREET: 6 Backer Farm Road
| CITY: Roseland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                        ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ATGCACAGCTGGGGAACAAGACG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 AAGCAGAGCGGTGGAACAAAGG 3
Lamparski, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                             NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WordPerfect 5
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ZIP: 07068-1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
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                                                                       Gaps
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                          Length 30;
                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: Windows SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                          Henderson, Daniel
TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/033,333
ATTORNEY/AGENT INFORMATION:
NAME: Catherine, Polizzi M
REGISTRATION NUMBER: 40,130
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION 1970-813-5600
TELEFRAX: 650-494-0792
                       55.8%; Score 13.4; DB 3; 73.9%; Pred. No. 6.3e+03; tive 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/614,495
FILING DATE: 11-Jul-2000
CLASSIFICATION: UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 755 PAGE MILL ROAD CITY: Palo Alto
                                                                                                                    2 ATGCACAGCTGGGGAACAAGACG 24
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                                                                                                                                                                 25 AAGCAGAGCGGTGGAACAAAGG 3
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; Sequence 18, Application US/09898883
; Patent No. 6885968
; GENEAL INFORMATION:
    APPLICANT: Little, Andrew
                                                                                                                                                                                                                                                                          Sequence 17, Application US/09614495
Patent No. 6436394
GENERAL INFORMATION
APPLICANT: Yu, De Chao
APPLICANT: Yu, De Chao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                   Ouery Match
Best Local Similarity 73.99
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: CA
                                                                                                                                                                                                                                    RESULT 36
US-09-614-495-17/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-614-495-17
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us-10-713-137-3.sizlim.rni

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TYPE: DNA
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Sequence 38, Application US/09814292

Sequence 38, Application US/09814292

GENERAL INFORMATION:

APPLICANT: Yu, De-Chao;

APPLICANT: Tanag, Hong

APPLICANT: Henderson, Daniel R.

TITLE OF INVENTION: HUAN UNCOPLATIOR EQUINCES, VECTORS COMPRISING

TITLE OF INVENTION: UROPLAKIN-SPECIFIC TRANSCRIPTIONAL REGULATORY SEQUENCES, AND

TITLE OF INVENTION: URFHODS OF USE THEREOF

TITLE OF INVENTION: URFHODS OF USE THEREOF

TITLE OF INVENTION: URFHODS OF USE THEREOF

TITLE OF INVENTION: URFHODS

CURRENT APPLICATION NUMBER: US/09/814,292

CURRENT FILING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 46

SEQ ID NO 38

LENGTH: 30

LENGTH: 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 55.8%; Score 13.4; DB 3; Length 30; Best Local Similarity 73.9%; Pred. No. 6.3e+03; Matches 17; Conservative 0; Mismatches 6; Indels
                APPLICATION NUMBER: US/08/462,159B
FILING DATE: 05-JUN-1995
CLASSIPICATION: 435
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,412
FILING DATE: 08-MAR-1994
ATTOWNEY ALGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFENCE/DOCKET NUMBER: 325800-440
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: PCR Primer 37.124.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ATGCACAGCTGGGGAACAAGACG 24
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US-09-875-228-24/c
'Sequence 24, Application US/09875228
'Patent No. 6916918
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                   TELECORIGES 201-994-1744
TELEPAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
CURRENT APPLICATION DATA
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APPLICANT: Henderson, D.R.
APPLICANT: Schuur, E.R.
TITLE OF INVENTION: A HUMAN GLANDULAR KALLIKREIN ENHANCER, VECTORS COMPRISING THE
TITLE OF INVENTION: BHIANCER AND METHODS OF USE THEREOF
TILE REFERENCE: 348022000900
CURRENT APPLICATION NUMBER: 09/127,834
FRIOR APPLICATION NUMBER: 09/127,834
FRIOR FILING DATE: 1998-08-03
FRIOR FILING DATE: 1998-08-03
FRIOR PILING DATE: 1998-08-04
FRIOR PILING DATE: 1998-08-04
FRIOR APPLICATION NUMBER: 60/076,545
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OTHER INFORMATION: produced synthetically.
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/cell_type="Embryonic stem cell"
/cell_line="ES cells 12952 (formerly 129/SvPas)"
/clone_lib="GGTC Gene Trap Library GV04C04"
/note="Vector: ROSAbetageo"
                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
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/clone="W255E01"
                                                                                                                                                                                                                                                                                                                                                                                                                                            sex="Male
     12904583
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                 DEFINITION
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COMMENT
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CL214453
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AL945338 Arabidops
AU103763 AU103763
AZ769231 1M0569G07
AI156750 ue54b07.r
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AZ511249 1M0356N10
AA958372 ualla03.r
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                                    December 13, 2005, 12:51:49; Search time 2984 Seconds (without alignments) 376.304 Million cell updates/sec
                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                            41078325 segs, 23393541228 residues
                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                             1 gatgcacagctggggaacaagacg 24
                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                          Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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AZ769231
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AU104109
AX555607
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                         - nucleic search, using sw model
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AZ511249
AA958372
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Match Length DB
                                                               US-10-713-137-3
                                                                                                                                                                                           9b_est1:*
9b_est2:*
9b_htc:*:
9b_est4:*
9b_est5:*
9b_est7:*
9b_gss2:*
9b_gss2:*
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      Copyright
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ROSAbetageot gene trap. Sequence tag generated by 5'RACE.
ROSAbetageot gene trap. Sequence tag generated by 5'RACE.
Additional sequence information can be found at:
'http://genetrap.gsf.de/project/web_new/database/result_clone.html?
clone id=W355B01' ES cell line harboring insertion mutation of
target gene is available at:
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm
l' Inhouse Sequence Identifier: 12462
                                                                                                                                                                                                                                                                                                                                                                JS DP MRNA linear GSS 22-MAR-2005 W255E01 GGTC Gene Trap Library GV04C04 Mus musculus cDNA clone W255E01, mRNA sequence.
          AZ814914 2M0082C24
BH855497 SALK 0850
BH656386 1007113H0
BH640991 1008039E0
CZ469449 C04702-3p
BM395302 50072-2-8
AA756443 zj50h10.8
AA7287473 z550h10.8
AA7287473 z55041.0
AA7287763 AV957763
AU7255694 AU255694
AA772767 AV957763
AU105506 AU105506
AU105506 AU105506
CZ90985 AU1011H1
DN955268 1E84h05.9
R10392 yf37e03.81
CC798667 SALK 1472
CC798667 SALK 1472
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi, Murcidea; Murinae; Mus.

1 (bases 1 to 38)
Hansen,J., Floss,T., van Sloun,P., Fuchtbauer,E.M., Vauti,F., Arnold,H.H., Schnutgen,F., Wurst,W., Von Melchner,H. and Ruiz,P. A large-scale; gene—driven mutagenesis approach for the functional analysis of the mouse genome
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
CW986355 KBrH012L0
                                                                                                                                                                                                                                                                     AG199766 Pan trod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Jan 27, 2005 this sequence version replaced gi:40731354
Contact: GGTC
                                                                                                                                                                                                                                                                                                          ALIGNMENTS
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: GGTC
German Genetrap Consortium (GGTC)
Email: info@genetrap.de
                                                                                              AJ239879
AA287473
AV957763
AU255694
AJ792767
AL254367
AU105507
CZ909855
                                                                                                                                                                                                                                                         AZ501408
AG199766
                                                           CZ469449
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                                    BH626386
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                                                                        BM395302
                                                                                   AA776443
                        BH855497
                                                BH640991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                 CL214453.2 GI:49489711
GSS.
                                    9998
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Rosso, M.C., Strizhov, N., Li, Y. and Weisshaar, B..

Rosso, M.G., Strizhov, N., Li, Y. and Weisshaar, B..

Direct Submission

L. Submitted (101-MAY-2004) Weisshaar B., Max-Planck-Institut fuer
Submitted (101-MAY-2004) Weisshaar B., Max-Planck-Institut fuer
Suchtungsforsching, Carl-von-Linne-Weg 10, Koolin, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.

It indicates an insertion close to or within gene At1g03160.

It indicates an insertion close to or within gene At1g03160.

Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project.

GABI-Kat is part of the German Plant Genomics program designated 'GABI-Kat in mpiz-Koeln.mpg.de/GABI-Kat/.

Information on line availability can be found at:

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /ecctype="Col-0" from DNA from Arabidopsis thaliana fnote="For was performed on DNA from Arabidopsis thaliana plants (TI) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(e) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
14756321
                                                                                                                                                                                                                                                                                                                                                CR396399 46 bp DNA linear GSS 01-MAY-2004
Arabidopsis thaliana T-DNA flanking sequence GK-198G05-025984,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana
Makaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, angnoliophyta; eudicotyledons, core eudicotyledons,
rosids, eurosida II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
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/clone="GK-198095-025984"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li.Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weisshaar, B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database the identification of T-DNA insertion mutants in Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
Weisshaar,B.
                     Length 37;
                                                                                   Indels
                     60.8%; Score 14.6; DB 9;
81.0%; Pred. No. 7.9e+04;
ive 0; Mismatches 4;
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12874060
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                                                                                                                                           4 GCACAGCTGGGGAACAAGACG 24
                                                                                                                                                                                   27 GCAGAGCTGGAGGACAAGTCG 7
                                                                                                                                                                                                                                                                                                                                                                                                                    genomic survey sequence
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                                                                                      17; Conservative
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                                                       Best Local Similarity
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                              Query Match
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AUTHORS
                                                                                      Matches
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TITLE
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KEYWORDS
SOURCE
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Weetor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources /documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|RR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                           GSS 20-FEB-2001
                                                                                                                                                                                                                                                                                                                       AZ812358
2M0112P10R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0112P10 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases I to 37)

Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Nouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center
                                                                Gaps
                                                             ö
   Length 38;
Query Match
62.5%; Score 15; DB 10; Length 38
Best Local Similarity 78.3%; Pred. No. 5.2e+04;
Matches 18; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.(
Plate: 0112 row: P column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0112P10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 37.
Location/Qualifiers
                                                                                                                        24
                                                                                                                                                                                7 ATTTAGAGCTGCGGAACAGGACG 29
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                                                                                                                        2 ATGCACAGCTGGGGAACAAGACG
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84112, US
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AZ832358/c
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19 bp DNA linear GSS 16-FEB-2001 1M0569G07R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIMO569G07 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                                                                                                                             AU103763 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HEP10745, mRNA sequence.
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
1 (bases 1 to 39)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Hominiator, Home.

Lobase 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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/db_xref="taxon:9606"
/clone=11p=10745"
/clone=11p="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.3%; Score 14; DB 1; Length 50; 77.3%; Pred. No. 1.5e+05; rive 0; Mismatches 5; Indels
                                       Length 38
                                                                                     5; Indels
                                         Score 14; DB 10;
Pred. No. 1.5e+05;
                                       DB 10;
                                                                                     0; Mismatches
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                                                                                                                                 1 GATGCACAGCTGGGGAACAAGA 22
                                                                                                                                                              33 GATGCACAACAGGCGATCACGA 12
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GSS.
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AU103763.1 GI:13553284
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                                         58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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                                                                                       17; Conservative
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Matches 17; Conserv
                                           Query Match
Best Local Similarity
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AZ769231/c
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Direct Submission

Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer

Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer

Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence has been recovered from the left border of the T-DNA.

It indicates an insertion within the locus defined by BAC clone

FSD14. Details on the protocols used for generation of the sequence

are described in References 1-3. The sequences are generated at the

MPI for Plant Breeding Research in the context of the GABI-Kat

project. GABI-Kat is part of the German Plant Genomics program

designated 'GABI'. Information on line availability can be found

at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
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/note="POC was performed on DNA from Arabidopsis thaliana plants (TI) which were transformed with the T-DNA from vector pAC16 (GenBank accession number: AJ537514). The lines contain one or more T-DNA inscrtions. The DNA fragment (s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the inscrtion. T-DNA derived sequences were removed."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
                                                                                                                                                                                                                                                                                                     AL945338 38 bp DNA linear GSS 01-APR-2004
Arabidopsis thaliana T-DNA flanking sequence GK-288F04-015346,
                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
Bukaryota, Viridplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis
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/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and Weisshaar,B.
High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
BioTechniques 35 (6), 1164-1168 (2003)
                                                                                            Gaps
                                                                                            ö
                                           Score 14.6; DB 11; Length 46;
Pred. No. 8e+04;
0; Mismatches 4; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Arabidopsis thaliana"
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12874060
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (thale cress)
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/db_xref="taxon:3702"
                                                                                                                                           2 ATGCACAGCTGGGGAACAAGA 22
                                                                                                                                                                                    45 Acecacaerecanana
                                                                                                                                                                                                                                                                                                                                                             genomic survey sequence
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                                                60.8%;
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                                                                         Similarity
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       ORIGIN
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//Jab.noil.em.RNA."

// Ab xref="Laxon:10090"

// Clone="IMAGE:1494901"

// Lissue_type="mammary gland"

// Lissue_type="mammary gland"

// Lissue_type="mammary gland"

// Lone lib="Soares mammary gland NMLMG"

// Lone lib="Soares mammary gland NMLMG"

// Lone lib="Soares mammary gland with a modified polylinker; lat strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), disested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CL844510

EX12606-5prime Drosophila melanogaster P{EPgy2} P element insertion lines Drosophila melanogaster genomic Sequence recovered from 5' end of P element, genomic survey sequence.
                             (bases 1 to 31)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Edopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

E 1 (Basea I to 38)
S Levis,R., Hoskins,R., Liao,G., Mozden,N., Tsang,G., He,Y.,
Karpen,G., Bellen,H., Rubin,G. and Spradling,A.
The Berkeley Drosophila Genome Project Gene Disruption Project
Unpublished (2001)
Berkeley Drosophila Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:932505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                           The WashU-HHMI Mouse EST Project Contact: Marara M/Mouse EST Project Contact: Marara M/Mouse EST Project WashIngton University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Pax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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  Sciurognathi; Muroidea; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.0%; Score 13.2; DB 1;
83.3%; Pred. No. 3.4e+05;
cive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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CL844510/c
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(http://www.jax.org/resources/
was hydrodynamically sheared by repeated passage through a
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwafe2 (gil 4732114|gblAF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Xiii0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Neselly, M., Rose, M., Rose, R., Stoken, R., Ingey, A., von Niederhausern, A. and Wright, D., Welse, R., Mouse whole genome scaffolding with paired end reads from 10kb Jasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, 184112, USA.
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                     rel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC1M0569G07"
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Location/Qualifiers
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                                                                                                                                                    The P element insertion position is base 31 in the 38 bases. This insertion position refers to the first base of the 8 base target recognition sequence. Class: transposon-tagged. Location/Qualifiers
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
                                                                                                                                                                                                                                                                                                                                                                                                             /note="Inverse PCR was performed on Drosophila melanogaster strains each of which contains one or more P{EPgy2} P-element transposon insertion. The resultant fragment for each strain was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://www.fruitfly.org/about/methods/inverse.pcr.html."
University of California, Berkeley
LSA Building, Berkeley, CA 94720-3200, USA
Fax: $106439947
Email: gerry@fruitly.berkeley.edu
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P
                                                                                                                                                                                                                                                                                               /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="texon:7227"
/clone lib="Drosophila melanogaster P{EPgy2} P element
insertion lines"
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Insert Length: 10000 Std Brror: 0.00
Plate: 0284 row: H column: 11
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Seg primer: CACACAGGAAACAGCTATGACC
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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High quality sequence stop: 41.
Location/Qualifiers
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Fax: 801 585 7177
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone llb="Mouse lokb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/G1 (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically shader or oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gpl|AP129072.1), a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complamentary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Xill0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1 (bases 1 to 43)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 612 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_fetal_lung_NbHL19W"
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/db_xref="taxon:10090"
/clone="UUGC1M0284H11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1743420"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GCACAGCTGGGGAACAAGACG 24
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AI185696.1 GI:3736334
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Homo sapiens
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Best Local Similarity 76.29
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50 bp mRNA linear EST 28-JAN-2004
AU103768 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP12651, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Hef-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshiromo-Dakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae, Homo.

1 (bases 1 to 50)

Suzuki,Y., Taira,H., Teunoda,T., Mizushima-Sugano,J., Sese,J.,
Suzuki,Y., Taira,H., Teunoda,T., Morishita,S., Okubo,K.,
Hata,H., Ota,T., 1sogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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/clone_lib="Sugano Homo sapiens cDNA library"
                                        Length 43;
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Pred. No. 4.4e+05;
0; Mismatches 5; Indels
    Score 13; DB 10; Lencard, No. 4.3e+05;
                         54.2%; Scor.
76.2%; Pred. No. 4...
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                            GATGAACAGATGTGGAAGATG 31
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AU104109.1 GI:13553630
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76.2%;
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Homo sapiens
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Best Local Similarity 76.2
Matches 16; Conservative
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1 (bases 1 to 50)
                                                                                        16; Conservative
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                                                                 Best Local Similarity
Matches 16; Conserv
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AU103768/c
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AU104109/c
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/mol_type="genomic DNA"
/wol_type="genomic DNA"
/dultivar="mixed background W23/A188/B73"
/tissue_type="leaf"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev stage="leaf"
/dev stage="leaf"
/dev stage="leaf"
/dev stage="lault"
/lab_host="DH108" - RescueMu (engineered from DB1ueScript backbone); Site_1: BamH1; Site_2: BglII;
/clone_lib="lill8" - RescueMu (engineered from pB1ueScript backbone); Site_1: BamH1; Site_2: BglII;
/note="Organ: laaf; Vector: RescueMu (engineered from pB1ueScript backbone); Site_1: BamH1; Site_2: BglII;
/note="Organ: laaf; Vector: RescueMu (engineered from units neements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid S was grown at San Diego in 2002. DNA was extracted from leaf strips, double digested using BamH1 and BglII; and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
1118044H12.2EL yl 1118 - RescueMu Grid S Zea mays genomic, genomic gurvey sequence.
CG803673
GSS 10-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
1 (bases 1 to 43)
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Tel: 650 723 2227
Fax: 650 725 8221
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/organism="Zea mays"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               23 GATGCCCCCGGGGGAAAAG 3
                                                                                                                                                                                                                                                                                                                                                         16; Conservative
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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Zea mays
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CG803673
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Best Local Similarity
Matches 17; Conserv
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/dev stage="asexual blood forms"
/dab_nost="saimiri boliviensis"
/lab_nost="saimiri boliviensis"
/clone lib="Pw MBN #16 (amplified twice)"
/note="vector: Lambda ZAP II (Stratagene); individual
/note="vector: Lambda ZAP II (Stratagene); individual
/notes excised into phagemid pBluescript; Site 1: EcoR I;
Site 2: EcoR I; Genomic DNA was prepared from asynchronous
blood stage forms of the Belem line of P. vivax grown in
squirrel monkeys. Parasitized erythrocytes were purified
                                                                                                                                                         Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Baritute of Medical Science
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Suzuki, Y., Construction and characterization of a full
Inength-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997)
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211PvA09 Pv MBN #16 (amplified twice) Plasmodium vivax genomic 3',
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 50)

Carlton,J.M.-R. and Dame,J.B.

The Plasmodium vivax and P. berghei gene sequence tag projects
Parasitol. Today 16 (10), 409 (2000)
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Dept. of Pathobiology, College of Veterinary Medicine
University of Florida
2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA
Tel: 352 392 4704
Fax: 352 392 9704
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/organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="taxon:9606"
/clone="HEP13777"
/clone_lib="Sugano Homo sapiens cDNA library"
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Pred. No. 4.4e+05;
0; Mismatches 5;
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/mol_type="genomic DNA"
/strain="Belem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: damej@mail.vetmed.ufl.edu
Seg primer: M13(-20) forward
Class: shotgun.
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         AUTHORS
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from contaminating host leukocytes by filtration of ADP activated blood through acid-washed glass beads and Whatman CF11 cellulose columns by gravity filtration. Purified DNA was digested with mung bean nuclease in the presence of 42.5% formanide at 500C as described (Galinski, M. et al. 1992. Cell 69,1213-1226, Vernick, K.D. et al. 1988. N.A.R. 16, 6883-6896). Eco RI linkers were added and the constructs ligated into Lambda ZAP II. P. vivax Belem was originally isolated from a patient in Belem, Brzzil 1980 by Mercia de Arruda, adapted to Saimiri monkeys by Jurg Gysin, and maintained since 1983 in squirrel monkeys."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BH865278 1inear GSS 05-AUG-2002 SALK 098078 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_098078, genomic survey sequence.
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/clone="SALK 098078"
/clone="SALK 098078"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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1 (bases 1 to 42)
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Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis Genome
Ontact: Joseph R. Ecker
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
Tionol N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Fax: 858 558 6379
Fax: 858 beguence recovered from the left border of This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At3g23970.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.2%; Score 13; DB 9; Length 50; 76.2%; Pred. No. 4.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Indels
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/mol_type="genomic_DNA"
/ecotype="Col-0"
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Arabidopsis thaliana
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Drosophila melanogaser (Interpretation Propose)

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neperata; Endopterygota; Drosophila.

Nopperata; Endopterygota; Drosophila.

Entydroidea; Drosophilae; Drosophila.

S Thibault, S.T.; Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A., Ryner, L., Cheung, L.M., Chong, A., Exickson, C., Fisher, W.W., Ryner, L., Hartouni, S.R., Howie, E., Jakkula, L., Joo, D., Killpack, K., Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, F., Swimmer, C., Kopczynski, C., Duyk, G., Winberg, M.L. and Margolis, J. A complementary transposon tool kit for Drosophila melanogaster using P and piggyBac
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H. Direct Submission
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC); 52, Oun-dong, Yusong-gu, Daejeon 305-313, Korea Center (GRC); (B-mail:redetoneemail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/, Tel:82-42-866-7181, Fax:82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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d01604-3prime Exelixis P element XP insertions Drosophila
melanogaster genomic Sequence recovered from 3' end of P element,
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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4018
Fax: 510 486 6798
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The P element insertion position is 1 in the 43 bases. This
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/clone_lib="RP-43 Chimpanzee Male BAC Library"
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Sequence orientation is forward strand relative to 5'
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db xref="taxon:9598"
/clone="RP43-082F17.T7"
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: EcoRI.
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CZ472331
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LIBRARY
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CZ472331/c
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                                                                                                                                                                                                                                                         AV812547 K. Sato unpublished cDNA library: Hordeum vulgare subsp. vulgare leaves vegetative stage Hordeum vulgare subsp. clone baakl2a18, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantea; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Hordeum.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Unpublished
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Pan troglodytes DNA, clone: RP43-082F17.T7, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2001)
Contact: Kazuhiro Sato
Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Email: kazasto@rib.okayama-u.ac.jp,
URL:http://www.rib.okayama-u.ac.jp/barley/
database:http://www.rib.okayama-u.ac.jp/barley/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barley EST sequencing project in NIG and Okayama Univ
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                                                                    GATGCACAGCTGGGGAACAAGACG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pan troglodytes (chimpanzee)
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AG200388.1 GI:45232563
GSS.
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AV832547.1 GI:14524636
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AV832547/c
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AUTHORS
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Gaps

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EST 18-MAR-1999

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/ tab nust="univb="
/clone lib="Sugano mouse kidney mkia"
/clone lib="Sugano mouse kidney mkia"
/note="Organ: Kidney; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); lst strand cDNA
was primed with an oligo(dT) primer
(ATGTGGCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pWE18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custow primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Glires; Rodentia;
Sciurognathi; Muroidea; Murinae; Mus.
Sciurognathi; Muroidea; Murinae; Mus.
S. (bases 1 to 49)
S. Marra, M., Hilliar, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Puderwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.
The Wabhu-NCI Mouse EST Project 1999
Conteat: Marra M/Wablu-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                          49 bp mRNA linear EST 18-MAR-1: uj28h01.yl Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1921297 5' similar to TR:Q61314 Q61314 APOLIPOPROTEIN B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                            Length 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 12.6; DB 1; Length 49; Pred. No. 6.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
                                                                               Indels
                            DB 10;
                            52.5%; Score 12.6; DB 10
78.9%; Pred. No. 6.6e+05;
iive 0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="IMAGE:1921297"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seg primer: custom primer used
High quality sequence stop: 1.
Location/Qualifiers
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/lab_host="DH108"
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/strain="C57BL"
                                                                                                                                     4 GCACAGCTGGGGAACAAGA 22
                                                                                                                                                                          26 GAACAGCTGGCGCAGAAGA 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI527771.1 GI:4441897
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sex="female"
                                                     Best Local Similarity 78.9
Matches 15, Conservative
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Best Local Similarity
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                                  Query Match
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LOCUS
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JOURNAL
COMMENT
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AUTHORS
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                                                                                                                                                                                           원
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                                                                                                                                                         /use trains broughting metanogasce.
/mol type="genomic w- strain"
/dtrain="isogenic w- strain"
/db_refe="wexton:7227"
/db_refe="wexton:7227"
/dlone lib="Exelixis P element XP (GenBank accession number / note="wector: P element XP (GenBank accession number / NYS15149); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. For the P element XP, we selected an easily mobilized ammunition element among inserts hopped onto the Binsinscy balancer. New insertions were collected in vials from dysgenic females using the standard chromosomal source of transposase, delta2-3. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AG217348 10 A7 bp DNA linear GSS 03-5EP-2002 Drosophila melanogaster DNA, clone:NP3335-5-1, flanking P{GaWB}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (27-AUG-2002) Shigeo Hayashi, RIKEN Center for Developmental Biology, Laboratory for Morphogenetic Singaling; Develow-ku, Minatojima-minamimachi 2-2-3, Kobe, Hyogo 650-0047, Japan (E-mail:shayashi@cdb.riken.go.jp, Tel:81-78-301-3184, Pax:81-78-301-3183)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone was isolated from genomic DNA flanking an insertion of the P element vector P{GaWB} of a Drosophila strain.
nsertion position refers to the first base of the 8 base target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashi, S., Ito, K., Sado, Y., Taniguchi, M., Akimoto, A., Takeuch Aigaki, T., Matsuzaki, F., Nakagoshi, H., Tanimura, T., Ueda, R., Uemura, T., Yoshihara, M. and Goto, S., GETDB, a database compiling expression patterns and molecular locations of a collection of Gal4 enhancer traps

2 (bases 1 to 47)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/clone="NP3335-5-1"
/note="flanking P{GaWB} transposon insertion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.5%; Score 12.6; DB 10; Length 43; 78.9%; Pred. No. 6.6e+05; ive 0; Mismatches 4; Indels (
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/mol_type="genomic DNA"
/strain="NP3335"
/db_xref="taxon:727"
/chromosome="2"
                                                                                                                                           organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (fruit fly)
                                  recognition sequence.
Class: transposon insertion site.
                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 ACAGCTGGGGAACAAGACG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 ACAGCTGACAACAAGCCG 4
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AG217348.1 GI:22764348
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AG217348/c
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Best Local Similarity 72.7%; Pred. No. 7.7e+05;
Matches 16; Conservative 0; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Wouse 10kb plasmid UUGCIM library"
/noce="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifica at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated by marses and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AF12972.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adapprored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Rammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.

E 1 (bases 1 to 25)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Lupublished (2000)

Lonpublished (2000)

Lonpublished (2000)

Lonpublished (2000)

Lonpublished (2000)

Lonpublished (2000)
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                                                                                                                                                                                                                             GSS 05-OCT-2000
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                                                                                                                                                                                                                      AZ511249
1M0356N10F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0356N10 F, genomic survey sequence.
       Gaps
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       Indels
       4.
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       Mismatches
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/mol_type="genomic DNA"
strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="tudGCIM0356NL0"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: (
Plate: 0356 row: N column: 10
Seg primer: CGTYGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 25.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
Mus musculus
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                                                     2 ATGCACAGCTGGGGAACAA 20
                                                                                    AZ511249.1 GI:10692565
       15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                        RESULT 21
AZ511249/c
LOCUS
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ORGANISM
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51.7%; Score 12.4; DB 9; Length 25;

Query Match

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AA958372 28 bp mRNA linear EST 08-MAY-1998 ualla03.rl Soares mammary gland NbwMG Mus musculus cDNA clone lmAc58:1346380 5' gimllar to TR:00111 00111 HYPOTHETICAL 28.2DA PROTEIN FROM HUMAN CHROMOSOME 19. [1] ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases I to 28)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marka M/Mouse EST Project
WashU-HMI Mouse EST Project
WashU-HMI Mouse EST Project
WashIngton University School of MedicineP
4444 Porset Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mousesestGwatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ifface considered overall poor quality
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seg primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/63"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="IMAGE:1346380"
22 ACGAGCAGCCGGGAACACAAC 1
                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
                                                                                                                                                                                                                AA958372.1 GI:3124602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 92.9
Matches 13; Conservative
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwalpa? (gil #712114 [gpl AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BH855497 linear GSS 08-JUL-2002 SALK 085040.16.20.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_085040.16.20.x, genomic
                                                                                                                                                                                                                                                                             E., SLC, UT
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Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse lokb plasmid UUGCIM library"
/note="Wector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                               plate: 0082 row: C column: 24
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="UUGC2M0082C24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 Argeacacacacacadadec 39
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                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
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nes 16; Conserv
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BH855497
LOCUS
DEFINITION
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                                                                                                                                                                                 CW986355 SETH, Brassica rapa HindIII BAC library Brassica rapa subsp. pekinensis genomic clone KBrH012L05, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pbeom@rda.go.kr
gequence of Brassica rapa ssp. pekinensis HindIII BAC clone
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                                                                                                                                                                                                                                                                                                                                                           Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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/lab_hogt="E.coli DH10B"
/clone lib="KBrH, Brassica rapa HindIII BAC library"
/note="Vector: pCUGIBac1; Site 1: HindIII; Brassica rapa
spp. pekinensis inbred line Chiffu BAC library (KBrH BAC)
is provided by Yong-Pyo Lim."
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2M0082C24R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0082C24 R, genomic survey sequence.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Brassica rapa subsp. pekinensis"
/mol type="genomic DNA"
/cultivar="Chiifu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Beom-Seek Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seedun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sub_species="pekinensis"
/db_xref="taxon:51351"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="KBrH012L05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BAC end sequence of Brae
KBrH012L05
Seq primer: M13 Reverse
Class: BAC ends.
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CW986355.1 GI:56852379
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AZ814914.1 GI:12984822
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                                       GATGCACAGCTGGG 14
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Best Local Similarity
Matches 13; Conserv
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JOURNAL
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CW986355
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JOURNAL

TITLE

FEATURES

REFERENCE AUTHORS

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/dlone lib="1007 - RescueMu Grid H"
/dlone lib="1007 - RescueMu Grid H"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site I: BamHI, Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.ramdb.isatate.edu' and follow the links for streacted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BH640991 49 bp DNA linear GSS 14-FEB-2002
1008039E08.1EL_x1 1008 - RescueMu Grid I Zea mays genomic, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1008039 row: 29
Class: transposon-tagged.
Location/Qualifiers
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/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / 1. 49 // Organism="Zea mays" // Organism="Zea genomic DNA" // Cultivar="mixed background W23/A188/B73" // Ab xref="taxon:4577" // tissue Lype="leaf" // tissue Lype="leaf"
                                                       /mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.7%; Score 12.4; DB 9;
72.7%; Pred. No. 8.2e+05;
tive 0; Mismatches 6;
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Department of Biological Sciences
Stanford University
                                  'organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="adult"
/lab_host="DH108"
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                                                                                                                                                                        /dev_stage="adult"
/lab_host="DH108"
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Walbot, V.
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Zea mays
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BH640991/c
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Contact: Walbot V
Stanfort V
Stanfort Office Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Fal: 650 723 2277
Pax: 650 725 8221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:3702"
/clone="SALK 08540.16.20.x"
/clone=lb="Arabidopsis thaliana TDNA insertion lines"
/clone=lbc="Rabidopsis thaliana TDNA insertion lines ach of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 bp DNA linear GSS 30-JAN-200;
1007113H06.1EL_x1 1007 - RescueMu Grid H Zea mays genomic, genomic
BH626386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bermatophyta, Magnollophyta, Liliopaida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; roaids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                       Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1007113 column: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At4g09190. Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                        Arabidopsis Genome
Unpublished (2001)
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@selk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /moi_type="genomic_DNA"
/ecotype="Col-0"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BH626386.1 GI:18439637
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

LOCUS

ACCESSION

RESULT 26 BH626386

Matches

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ORIGIN

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Gape

us-10-713-137-3.sizlim.rst

ORIGIN

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Drosophila melanogaster (fruit fly)

Brosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;

Bukaryota; Bracaoa; Arthropoda; Haxapoda; Insecta; Pterygota;

Bobydroidea; Drosophila.

E 1 (bases 1 to 49)

E 2 (bases 1 to 49)

E 3 (base 1 to 49)

E 3 (base 1 to 49)

E 4 (base 1 to 49)

E 4 (base 1 to 49)

E 4 (base 1 to 49)

E 5 (base 1 to 49)

E 6 (base 1 to 49)

E 7 (base 1 to 49)

E 7 (base 1 to 49)

E 7 (base 1 to 49)

E 8 (base 1 to 49)

E 9 (base 1 to 49)

E 1 (ba
                     Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web salte www.zmdb.isstate.edu and follow the links for 'RescueMu', Grid I was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and Bgill, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
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designed to allow plasmid rescue from total genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CO4702-3prime Exelixis piggyBac PB insertions Drosophila melanogaster genomic Sequence recovered from 3' end of piggyBac, genomic survey sequence.
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The piggyBac insertion position is 1 in the 49 bases. This insertion position refers to the first base of the 4 base TTAA target recognition sequence.
Class: transposon insertion site.
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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Fax: 510 486 6798
Fax: 10 486 6798
Fax: method was inverse PCR.
Sequence recovery method was inverse PCR.
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/mol type="genomic DNA"
/strain="isogenic w- strain"
/db xref="taxon:722"
/clone_lib="Exelixis piggyBac PB insertions"
/clone_lib="Exelixis piggyBac PB insertions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 12.4; DB 9; Length 49; Pred. No. 8.2e+05;
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Best Local Similarity
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CZ469449
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transposase expression by immersing bottles in a circulating 370C water bath for a daily (days 3-10 after egg-laying) 1-h heat shock. We outcrossed the resulting dysgenic males to an isogenic w- strain. New insertions were identified on the basis of a change in eye color (third chromosome ammunition) or the appearance of w+ male progeny (X chromosome ammunition). All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."
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/db_xref="raxon:5911"
/clone lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 18)

Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Terrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
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Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BM395302
50072-2-8-E01.r.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                         1; Indels
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/organism="Tetrahymena thermophila"
/mol type="mRNA"
/strain="CU428.1"
                                                                                                                                                                                                                                                                            Score 12.4; DB 10;
Pred. No. 8.2e+05;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: apturkew@midway.uchicago.edu
Seq primer: T3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 ACAGCTGGGGGCCCAGA 1
                                                                                                                                                                                                                                                                              51.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                11 recacaccreesea 24
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Best Local Similarity 92.9
Matches 13, Conservative
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Fax: 773 702 3172
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nes 14; Conserv
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AA776443/c
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BM395302/c
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14; Conservative
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AA287473
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AJ239879 Aspergillus niger ATCC6275 Aspergillus niger CDNA clone
AJ239879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Fungl, Ascomycota, Pezizomycotina, Eurotiomycetes, Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus, (bases I to 37)
Choi, J.Y., Lee, D.W., Koh, J.S., Kim, J.H., Yang, M.S. and Chae, K.S. Identification of expressed sequence tags (ESTs) of the highly
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                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
Euarchontoglires; Primates; Catarrhini;
                                                                                                                                 1 (bases 1 to 36)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kroaba, T., Lary, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                     Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 50.8%; Score 12.2; DB 1; Length 36; Best Local Similarity 82.4%; Pred. No. 9.9e+05; Matches 14; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .36
/organism="Homo sapiens"
/ol_type="mRNA"
/db_xref="GDB:1390119"
/db_xref="taxon:9606"
/clone="IMAGE:453763"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 CAGCTGGGGAACAAGAC 23
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                   GI:2835777
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                                                  Homo sapiens (human)
                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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Aspergillus niger
                                                                                                                                                                                                                                       Unpublished (1997)
                                                                                                                       Hominidae, Homo.
                                                                      Homo sapiens
AA776443
AA776443.1
               VERSION
KEYWORDS
SOURCE
ORGANISM
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AJ239879
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/mol type="mRNA"

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/db_xref="mRNA"

/db_xref="mRNA"

/db_xref="mRNA"

/db_xref="mRNA"

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/clone="type="germinal center B cell"

/lab host="mland"

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/lab host="mland"

/clone lib="NCI CGAP GCB!"

/clone lib="nci cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), gravided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). CDNA synthesis was primed with a Not I - oligo(dT) primer

/corrected for gerald warti (CBER). CDNA synthesis was primed with a Not I - oligo(dT) primer

/corrected for gerald warti (CBER). CDNA synthesis was primed with a Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 bp mRNA linear EST 13-AUG-1997 similar to dbj|D16558|SCJRDNA Scytosiphon lomentaria rDNA for 188, 5.88 and 25S (rRNA);, mRNA sequence.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Tumor Gene Index

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Infis clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Trace considered overall std Error: 0.00
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
transcribed genes in Aspergillus niger
Biotechnol. Lett. 21, 381-384 (1999)
Contact: Chae KS
                                                                                                                                                                                                                       1. .37
/organism="Aspergillus niger"
                                                                                        Faculty of Biological Sciences
Chonbuk National University
Chonju 561-756, Republic of Korea.
Location/Qualifiers
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EST.
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45 bp mRNA linear EST 08-DEC-2004 01792767 Antirrhinum majus cDNA clone 018 2 12 108, mRNA sequence. AJ792767 1 GI:51108095 EST.
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Antirrhinum majus
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Lamiales; Plantaginaceae; Antirrhineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antirrhinum.

(bases 1 to 45)

Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H.,
Saedler,H. and Zachgo,S.
Characterization of Antirrhinum Petal Development and
Identification of Target Genes of the Class B MADS Box Gene
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                   /tissue type="brain"
/clone_lib="3'-directed mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Antirrhinum majus"
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/clone_Tib="Antirrhinum majus whole plant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
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Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
1016.5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5589
Fax: 81-743-72-5589
Email: kkato@bs.aist-nara.ac.jp,
URL:http://love2.aist-nara.ac.jp/BED/index.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molekulare Pflanzengenetik
MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant Cell 16 (12), 3197-3215 (2004)
                                                                                                                                                                                          /organism="Mus musculus"
                                                                                                                                                                                                            /mol_type="mRNA"
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/clone="BED0006185"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Schwarz-Sommer Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 CAATTGGGGAACAGGAC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 AGCTGGGGAACAAGACG 24
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PUBMED
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                                                                                                                                                                                                                                                                                         EST 14-MAR-2002
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1 (Basea I to 42).

Satoh, M., Satou, Y., Kohara, Y. and Shin-i, T.

Expressed genes in Ciona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Contact: Nori Satoh
Kyoto University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.

1 (bases 1 to 44)

Kato, K. and Matoba, R.
Generation of expressed sequence tags from mouse brain Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library, egg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                    Gaps
   went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                       AV957763 AV9577763 Nori Satoh unpublished cDNA library, egg Ciona intestinalis cDNA clone cieg05k15 5', mRNA sequence. AV957763
                                                                                                                    ö
                                                                             ch 50.8%; Score 12.2; DB 1; Length 41; I Similarity 82.4%; Pred. No. 1e+06; 14; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: satch@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
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/organism="Ciona intestinalis"
/mol type="mRNA"
/db xref="taxon:7719"
/clone="cieg05k15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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Mus musculus
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Ciona intestinalis
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KEYWORDS
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AU255694/c
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Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ins.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugamo,S. Construction and characterization of a full
1-length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AU105507 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HRC12884, mRNA sequence.
                                                                                                                                                                                              Department of Virology
Institute of Medical Science, University of Tokyo
1-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
1-6-1, Shirokanedai, Minatoku, Tokyo 208-8639, Japan
1-6-1, Shirokanedai, Minatokyo. Isaacip
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Suzuki,Y. Tatra,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="HRC12884"
/clone_lib="Sugano Homo sapiens cDNA library"
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/db_xref="HRC12806"
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82.4%; Pred. No. 1e+06;
iive 0; Mismatches 3;
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                                                                                                                                                                            Contact: Yutaka Suzuki
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/clone_lib="NCI_CGAP_Ov31"
/note="Toragan: ovary; Vector: pAMP1; mRNA made from ovarian carcinoma, cDNA made by oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Non-amplified library. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tisaue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuaqui,
Tisaue Procurement: W. Marston Linehan, Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium, LiNL

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at:

www-bio.llnl.gov/bbrp/image/image.html
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qv33a10.x1 NCI CGAP Ov31 Homo sapiens cDNA clone IMAGE:1983354 3'
similar to gb:L21696 cds1 PROTHYMOSIN ALPHA (HUMAN);contains
TAR1.t1 TAR1 repetitive element ;, mRNA sequence.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini; Hominidae, Homo.

1 (Dases 1 to 49)

NCI-CRAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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AI254367.1 GI:3861892
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1 (bases 1 to 50)
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Unpublished (1997)
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Search completed: December 13, 2005, 15:51:25 Job time : 2988 secs
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/lab.host="blub108"
/clone lib="4018 - RescueMu Grid X"
/clone lib="4018 - RescueMu Grid X"
/clone lib="adult"
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Contact: Walbot V
Department of Biological Sciences
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855 California Ave, Palo Alto, CA 94304, USA
855 California Ave, Palo Alto, CA 94304, USA
855 California Ave, Palo Alto, CA 94304, USA
865 California Ave, Palo Alto, CA 94304, USA
8221
8mail: walbot@stanford.edu
Verý probable ligation site of ends cut by single endonuclease.
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/organism="Zea mays"
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Gnetophyta; Gnetophia; N.N., O'Shaughnessy, A.L., Balija, W., Martienssen, R.A., McCombie, R.W., Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Hazbor Laboratory
PO Box 100, Cold Spring Hazbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 267 8814
Fax: 516 267 8814
Fax: 516 267 8814
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/note="Organ: mature, unfertilized reproductive strobili;
/notes="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express CDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #416/84"
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/organism="Gnetum gnemon"
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/db_xref="taxon:3382"
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DN955268.1 GI:63027406
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Human GDM

Aaq53128 Gene dete
Aav28684 Probe for
Aav20056 N-ras pro
Aav73038 Human ras
Aav73141 Human ras
Adj22962 Human end
Adj22962 Human end
Adj22961 Human end
Adj23531 Human end
Adj23531 Human end
Adj23531 Human GDM
ADN1337 Human GDM
ADN1376 Human GDM
ADN1376 Human GDM
ACN76465 Human GDM
ACN76461 Human GDM
ACN76467 Human GDM

ADJ23531

Title:

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se; PCR; high altitude pulmonary edema; pulmonary edema;
respiratory-gen.; respiratory disease; SNP detection; allelic variation;
primer; exon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting predisposition to high altitude pulmonary edema (HAPE) by amplifying intron 7 of human inducible nitric oxide synthase gene, and predicting and analyzing differences in the distribution of allelic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel method for detecting predisposition thigh altitude pulmonary edema (HAPE). The method comprises amplifying intron 7 of the human inducible nitric oxide synthase (iNOS) gene (ADZ75764) by designing and synthasizing forward and reverse oligonucleotide primers (ADZ75765), and predicting and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human inducible nitric oxide synthase gene exon 7 reverse PCR primer.
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Adr77767 Livin RNA
Aad05966 Human dia
Abr76929 Blocking
Adf72069 Human XPC
Ads74065 Tumour su
Abz30347 Candida a
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Abz06403 Human leu
Abz06793 Human leu
Abn08477 Human GDM
Acc52706 Human tum
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Abz06705 Human leu
Abz07095 Human leu
Aal47160 S pneumon
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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                                                                                                                                                         ö
statistically analyzing differences in the distribution of the allelic variants in the populations, where GG genotype at 19480 position are at low risk of HAPE, and AA genotype at 19480 position are at hAPE. The present sequence represents the forward oligonucleotide primer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New beta-actin and ribosomal protein S21 (rpS21) promoters, useful as enhancers and repressors for expression of heterologous nucleic acids encoding therapeutic proteins such as approximatelya-glucosidase, antibodies, and insulin.
                                                                                                                                                         Gaps
                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                    Forward primer for PCR of chinese hamster beta-actin promoter.
                                                                                                                              DB 14; Length 24;
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                                                                                                                                                                                                                                                                                                                                                                                                 Primer; 88; DNA amplification; PCR; beta-actin promoter.
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                                                                                                  Seguence 24 BP; 8 A; 5 C; 9 G; 2 T; 0 U; 0 Other;
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100.0%; Pred. No. 0.2
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; SEQ ID NO 35; 95pp; English.
                                                                                                                                                                                     1 GATGCACAGCTGGGGAACAAGACG 24
                                                                                                                                                                                                       GATGCACAGCTGGGGAACAAGACG 24
                                                                                                                                                                                                                                                                                    BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUN-2004; 2004WO-US017422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-JUN-2003; 2003US-0480768P
                                                                                                                                                                                                                                                                                    ADW69302 standard; DNA; 26
                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                            Local Similarity 100.
nes 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENZ ) GENZYME CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-058125/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang W;
                                                                                                                                                                                                                                                                                                                                                                                                                             Cricetulus griseus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2005000888-A2.
                                                                                                                                                                                                                                                                                                                                           24-MAR-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Estes SD,
                                                                                                                                                                                                                                                                                                                ADW69302;
                                                                                                                                Query Match
                                                                                                                                                            Matches
                                                                                                                                                                                                                                                          RESULT 2
                                                                                                                                                                                                                                                                         ADW69302
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65.0%; Score 15.6; DB 14; Length 26; 81.8%; Pred. No. 2e+03;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Korean hepatitis C virus antigenic proteins - comprising epitopes of core protein, non-structural proteins or envelope protein, used for
                                                                                                                                                                                                                                                                                                            E2A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Livin RNA used to prepare siRNA for therapy-resistant tumour therapy.
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                                                                                                                                                                                                                                                                                                        Korean-type hepatitis C virus; KHCV; HCV; envelope protein; E2E; epitope; diagnosis; primer; polymerase chain reaction; amplification; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15; DB 2; Length 38;
Pred. No. 3.9e+03;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kim IS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 38 BP; 4 A; 12 C; 10 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yang JY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 gergaacagergegaaacacae 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 27; 91pp; English.
23
                                  22
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  2 ATGCACAGCTGGGGAACAAGAC
                                      1 AGGCCCAGCTTGGGACCAAGAC
                                                                                                                                     BP
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                                                                                                                                                                                                                                                                         KHCV envelope primer PEIEGT2
                                                                                                                     734/c
AAQ74734 standard; cDNA; 38
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                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kim CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Les 18; Conservative
                                                                                                                                                                                                                (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LUCK-) LUCKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Choi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-NOV-1994.
                                                                                                                                                                                                                25-MAR-2003
26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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Best Local S:
                                                                                                                                                                            AAQ74734;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADT77767/c
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                                                                                                                       AAQ74734/
                                                                                                   RESULT 3
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Human diacylglycerol kinase-zeta intron 22/exon 23 junction sequence.

(first entry)

31-JUL-2001

AAD05966;

AAD05966 standard; DNA; 20 BP.

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The present sequence corresponds to nucleotides 611-629 of the coding sequence of the livin (inhibitor of apoptosis protein) gene. Use of a nucleic acid containing this sequence, or its fragment of derivative, to prepare siRNA which sensities therapy-resistant tumour calls for a poptosis is claimed. The siRNA is preferably delivered into a therapy-resistant tumour calls for using liposomes or hydrodynamic injection. The siRNA will be present sequence joined, via a linker, to a complementary DNA strand. This is also used to prepare siRNA which sensities therapy-resistant tumour cells for apoptosis, and is inserted into an expression vector with a cytostatic compound, death receptor ligand, death receptor into an expression vector with a cytostatic compound, death receptor ligand, death receptor into an expression vector with a cytostatic compound, death receptor ligand, death receptor into an expression vector anchor in sentiobdy or negative regulator of anni-appoince proteins. The therapy are sistant tumour is neuroblastoma, intestinal carcinoma preferably colon, familiary adenomatous polyposis, hereditary non-polyposis colorectal. Oesophagasi, labial, laryngeal, hypopharynx, salivary and colorectal acarcinoma, medullary thyroid carcinoma, senior and preference carcinoma, service arcinoma, serviced carcinoma, serviced carcinoma, serviced carcinoma, becast carcinoma, serviced carcinoma, becast carcinoma, astrocycoma, menance carcinoma, nearonoma, panceatic carcinoma, medullary deponential carcinoma cervice preferably glioblascoma, astrocycoma, meningioma, medullary continuar carcinoma, service may use partice may all pladder carcinoma, uterine carcinoma, medullary continuary carcinoma, melanoma, burkitt's lymphoma, acute lymphatic leukaemia (CML), acute myeloid leukaemia (AML), chronic carcinoma, pania parenchyma, multiple myelond, paperocalmy sensitiona, cervical carcinoma, bronchial carcinoma, sellongarioma, carcinoma, pania sarcinoma, bronchial carcinoma, sellongarioma, choroidea melanoma, melanoma, labader c
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of a nucleic acid, or its fragment or derivative, for preparing Livin -specific siRNAs as an apoptosis inhibitor for the treatment of therapy-
Livin; inhibitor of apoptosis protein; short interfering RNA; siRNA; RNAi; gene silencing; cytostatic; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                            Crnkovic-Mertens I, Hoppe-Seyler F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carcinoma or melanoma (all claimed).
                                                                                                                                                                                                                                                                                                             (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 1; 22pp; English.
                                                                                                                                                                                                                   15-APR-2003; 2003EP-00008081
                                                                                                                                                                                                                                                                 15-APR-2003; 2003EP-00008081
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-730758/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        resistant tumors.
                                                                            Homo sapiens
                                                                                                                        EP1469070-A1
                                                                                                                                                                      20-OCT-2004.
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                        Score 14.4; DB 13; Length 19;
Pred. No. 6.9e+03;
0; Mismatches 1; Indels
Sequence 19 BP; 2 A; 7 C; 5 G; 0 T; 5 U; 0 Other;
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                          60.0%;
                                                                              ACAGCTGGGGAACAAG 21
                                                                                                      16 ACAGCTGGGGAACCAG 1
                                                    Conservative
                                  Local Similarity
Les 15; Conserv
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Matches
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AAD05966/c RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                namely diacylglycerol kinase epsilon, diacylglycerol kinase zeta, diacylglycerol kinase zeta-2 and their corresponding CDNAs. Human diacylglycerol kinase DNA is useful for coding human diacylglycerol kinase, which is useful for catalysing the conversion of diacylglycerol to phosphatidic acid. In particular, the human diacylglycerol kinase and its DNA are useful for decreasing intracellular levels of diacylglycerol [DAG) and for increasing intracellular levels of diacylglycerol glycerol (DAG) and for increasing intracellular levels of phosphatidic acid in cells. The present DNA sequence is the exon/intron junction sequence of human diacylglycerol kinase (DGK) zeta gene
                                                                                                  Human; catalyst; diacylglycerol; DAG; phosphatidic acid; DAG modulator; diacylglycerol kinase zeta; DGK; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New DNAs of the human diacylglycerol kinase, useful for modulating the levels of diacylglycerol kinase in cells to catalyze the conversion of diacylglycerol to phosphatidic acid, therefore increasing phosphatidic acid levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The patent discloses novel human diacylglycerol kinase (DGK) isoforms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Topham M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Col 17-18; 74pp; English.
                                                                                                                                                                           cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABV76929 standard; DNA; 30 BP.
                                                                                                                                                                                                                                                                                                                                                                                                 96US-0016210P.
97US-00841483.
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/partial
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/number= 22
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/*tag=
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prescott SM,
                                                                                                                                                    Homo sapiens
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ID ABV7
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New nucleic acid encoding a p53 variant that can transactivate p21- and 14-3-3 sigma-promoter but not e.g. the PIG3-promoter, for obtaining complementary sequences capable of inhibiting expression of p53 variant and treating tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a method for determining whether an age can be used to reduce the proliferation and/or cause the death of cance cells or inhibit the growth of a cancer cell population. The method is useful in determining whether an agent can be used to reduce the proliferation and/or cause the death of cancer cells or inhibit the growth of a cancer cell population. The present sequence represents a P primer which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                       Determining whether an agent can be used to reduce the proliferation, cause the death or inhibit the growth of cancer call population by obtaining a sample of cancer cells and quantifying the level of expression of a marker in the cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour; suppressor; p53; splice variant; cytostatic; gene therapy;
diagnosis; RT-PCR; primer; 88.
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                                                                                                                                                                                                                                                                         Demuth JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 14.4; DB 10; Length
Pred. No. 7.7e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 42 BP; 4 A; 14 C; 6 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                         Warner KA, Graves TG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                            27-MAR-2003; 2003WO-US009428
                                                                                                                 28-MAR-2002; 2002US-0368288P.
28-MAR-2002; 2002US-0368409P.
                                                                                                                                                                                                                (MEDI-) MEDICAL COLLEGE OHIO
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nes 18; Conservative
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                                                                                                                                                                                                                                                                         Weaver DA,
                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-902899/82.
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Crawford EL;
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09-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The specification describes a nucleic acid synthesis reaction of selected regions of target nucleic acids from a group of two different target nucleic acids from a group of two different target different target nucleic acids. The method comprises combining in a reaction mixture, two different target nucleic acids, polymerase, additionally combining a blocking agent capable of binding a nucleic acid template molecule so template, and exposing the reaction mixture to a template acids are synthesized by the polymerase. The method is useful for nucleic acid synthesized by the polymerase. The method is useful for nucleic acid synthesize by the polymerase. The method is useful for uncleic acid synthesized by the polymerase. The method is useful for uncleic acid synthesized his terminal polymerase. The method is useful for used in the method of the invention to block amplification of the chymotrypsin B precursor. The oligonucleotides are used to demonstrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proliferation; cancer; cancer cell growth inhibition; human; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preferential nucleic acid synthesis reaction of selected regions of target nucleic acids, by using a blocking agent which preferentially binds templates which are not desirable when amplifying the nucleic
                                                                                                 Nucleic acid synthesis; blocking agent; polymerase; DNA library; chymotryptin B precursor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.0%; Score 14.4; DB 8; Length 30; 75.0%; Pred. No. 7.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                            Blocking oligonucleotide #5 for chymotrypsin B precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 30 BP; 9 A; 2 C; 15 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human XPC gene PCR primer SEQ ID NO:36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GATGCACAGCTGGGGAACAAGACG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATGCACGGAGGGAGGAAGAGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 6; 20pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                    24-APR-2001; 2001EP-00109971
                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-APR-2001; 2001EP-00109971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LION-) LION BIOSCIENCE AG.
(first entry)
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Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kranz H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-077619/08
                                                                                                                                                                                                                                                                            EP1253205-A1
   03-MAR-2003
                                                                                                                                                                                                                                                                                                                                        30-0CT-2002
                                                                                                                                                                                                                   Synthetic.
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The present sequence is that of RT-PCR primer E11R for the p53 tumour suppressor gene. RT-PCR was used to detect possible alternative splicing of p53 in different primate cell lines. A novel isoform of p53 (deltap53) was identified that is generated by alternative exon splicing. RT-PCR showed that deltap53 lacks 198 nucleotides from exons 7, 8 and 9. The calcution contains a donor site-like splicing-cassette within the coding exon 7 (nucleotide 767) and an acceptor site-like splicing-cassette within the coding exon 9 (nucleotide 965). The resulting transcript contains a unique junction of exon 7 with 9, which does not alter the open reading frame. Thus, the novel p53-isoform lacks 66 amino acid residues from the central portion and hinge region of the protein but includes the functionally important C-terminal domain. The 984 bp transcript of deltap53 is found in human, African green monkey and Rhesus monkey. Unlike full-length p53, the p53 splice variant is capable of transcripting the endogenous p21 and 14-3-3sigma promoter but not the money. Date of the p53 variant, using antisense RNA or a ribozyme, for cancer therapy. Diagnostic compositions comprising a probe for detection of the splice variant are also claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
signal transduction; DNA replication; cell division; growth;
proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to constructing (M1) a strain of diploid fungal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.2%; Score 14.2; DB 13; Length 21; 84.2%; Pred. No. 8.7e+03; ive 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 36; SEQ ID NO 4498; 167pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Candida albicans GRACE strain PCR primer SEQ ID NO 4498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohlsen KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21 BP; 7 A; 4 C; 8 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.2%; Prec. N. Strive 0; Mismatches
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                  Example 1; SEQ ID NO 17; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GCACAGCTGGGGAACAAGA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boone C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABZ30347 standard; DNA; 22 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-DEC-2000; 2000US-0259128P.
20-FEB-2001; 2001US-00792024.
22-AUG-2001; 2001US-0314050P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-DEC-2001; 2001WO-US049486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-566694/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUL-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an companiation, of a promoter replacement by a cassette having an recombination, of a promoter replacement fragment with a heterologous promoter. (MI) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The diploid fungal cells in which both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian compound catabolism, blosynthetic, treatment of a mammalian catabolism, blosynthetic, treatment of a mammalian compound catabolism, blosynthetic, transporter, transcriptional, signal transduction, DNA replication and cell division activity. The method is useful for identifying a compound having the compound catabolism, blosynthetic, transporter, transcriptional, signal transduction, DNA replication and cell division activity. The method is useful for identifying a compound having the cativity to inhibit growth or proliferation of C. albicans cells and for treating infection by C. albicans. The presente sequence is that of a PCR or primer used in the method of the invention. Note: The sequence data for this parametric information and parametric or parametric properented in the present sequence and parametric or activity or inhibit growth or provent or parametric by parametric provents or parametric by the parametric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutation factor; chromosome 10; glioma; tumour suppressor; tumour; astrocytoma; gene therapy; human; mouse; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 59.2%; Score 14.2; DB 6; Length 22; Best Local Similarity 84.2%; Pred. No. 8.7e+03; Matches 16; Conservative 0; Mismatches 3; Indels
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yseful in the diagnosis and gene therapy of brain tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22 BP; 6 A; 2 C; 9 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nerve mutation factor DNA amplifying primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saya
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; Page 25; 78pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SUME ) SUMITOMO ELECTRIC IND CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GATGCACAGCTGGGGAACA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATGGAGAGCTGGTGAACA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX77148 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-347474/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nerve mutation
brain tumour; a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakata M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX77148;
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The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
                                                                                                                                                                                                   17, leukocyte; gene expression profiling; allograft rejection;
atherosclerosis; congestive heart failure; systemic lupus erythematosus;
rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             muth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J, Woodward R, Quertermous T, Johnson F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human leukocyte gene expression profiling probe SEQ ID NO 7086.
                                                                                                                                                              Human leukocyte gene expression profiling probe SEQ ID NO 6696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 14.2; DB 6; Length 50;
Pred. No. 9.8e+03;
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                                          ABZ06705 standard; DNA; 50 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                        22-OCT-2001; 2001WO-US047856.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-OCT-2000; 2000US-0241994P. 08-JUN-2001; 2001US-0296764P.
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                                                                                                                          (first entry)
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ABZ07095 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BIOC-) BIOCARDIA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-636525/68.
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                                                                                                                                                                                                                                                                                                                                                         WO200257414-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wohlgemuth J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JAN-2003
                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                          09-JAN-2003
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                                                                                   ABZ06705;
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Matches
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RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABZ07095,
                       ABZ06705
                                                            g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding a bio catalyst which desulphurises fossil fuels - obtd, from Rhodococcus rhodochrous bacteria, used to produce microorganisms which degrade organic sulphur cpds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA obtained from Rhodococcus rhodochrous encodes enzymes/biocatalysts which can desulphurise fossil fuels (See AAG51131, AAG55132).
Microorganisms transformed with the DNA can be used to produce the enzymes/biocatalysts for the selective oxidative cleavage of carbonsulphur bonds for desulphurisation of fossil fuels which contain organosulphur compounds. Two primers (AAG55125, AAG55125) were used to amplify the sequence designated as open reading frame 1 (ORF 1) of the DNA descibed in AAG55131. (Updated on 25-MAR-2003 to correct PN field.)
  (AAY21558 and AAY21559) are provided. The protein is believed to have tumour suppressor activity. Polymuclectide sequences and antibodies to the protein are diagnostic reagents for highly malignant brain tumors such as astrocytoms where chromosome 10 deletion commonly occurs. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer for sequence coding enzymes which desulphurise fossil fuel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Denome
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                                                                                                                                                                  Score 14.2; DB 2; Length 23; Pred. No. 8.8e+03;
                                                                                                                                                                                                           3, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Young KD,
                                                                                     gene may also be used for gene therapy of such tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enzyme; biocatalyst; fossil fuel; oxidation; cleavage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 37 BP; 8 A; 8 C; 12 G; 9 T; 0 U; 0 Other;
                                                                                                                              Sequence 23 BP; 2 A; 6 C; 8 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piddington CS, Kovacevich BR,
                                                                                                                                                                                                             0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 5; Page 61; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organosulphur compounds; coal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GCACAGCTGGGGAACAAGA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 CACAGCTGGGGAACAAGAC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ENER-) ENERGY BIOSYSTEMS CORP.
                                                                                                                                                                                                                                                                                19 CCCAGCTGAGGAACAAGCC 1
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                                                                                                                                                                     59.2%;
84.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
(first entry)
                                                                                                                                                        Query Match
Best Local Similarity 84.29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1994-035068/04.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JUL-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-JUL-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
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02-AUG-1994
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AAQ55126;

RESULT 11 AA055126

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Human genome, biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; diagnosis; single nucleotide polymorphism; SNP; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel biallelic markers used to construct a high density disequilibrium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ65654 to AAZ69578 represent human biallelic markers from the present
                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of a Streptococcus pneumoniae surface protein, called SpsA, that binds to secretory 1gA The sequences can be used in vaccines for treating pneumococcal infections. The present sequence is a PCR primer used to isolate the coding sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                             Pneumococcal surface protein SpsA - for use in producing vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/standard_name= "single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                               ch 58.3%; Score 14; DB 2; Length 37; 1 Similarity 77.3%; Pred. No. 1.2e+04; 17; Conservative 0; Mismatches 5: Indele
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 37 BP; 12 A; 10 C; 13 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human map-related biallelic marker SEQ ID NO:1997.
                                                          (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chumakov 1;
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replace (24,G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GATGCACAGCTGGGGAACAAGA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 656; 2745pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 6; Page 5-6; 12pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                    97DE-01008537.
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                                                                                                  Hammerschmidt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ67650 standard; DNA; 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 map of the human genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-013267/01
                                                                                                                                       WPI; 1998-481924/42
                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9954500-A2
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                    03-MAR-1997;
                                                                                                Chhatwal GS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ67650;
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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T7; leukocyte; gene expression profiling; allograft rejection; atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pneumococcal; surface protein; secretory IgA; vaccine; infection;
                                                                                                                                                                                                                                                                                                                                                                 Phillips J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.2%; Score 14.2; DB 6; Length 50; 84.2%; Pred. No. 9.8e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                   Altman P, Prentice J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 50 BP; 10 A; 15 C; 9 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                   muth J, Fry K, Matcuk G, Altman P, P
Woodward R, Quertermous T, Johnson F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S pneumoniae SpsA gene PCR primer SH24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 556; Opp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                               20-OCT-2000; 2000US-0241994P.
08-JUN-2001; 2001US-0296764P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                           (BIOC-) BIOCARDIA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-636525/68.
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                                                                                                                                                                                                                                                                                                                                                                   Wohlgemuth J,
                                                                                                                                         WO200257414-A2
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                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-SEP-1998.
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invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ77440 represent amplification primers for the biallalic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and disgnostic methods, as well as the characterisation of the pharmaceutical agents acting on a disease as well as other treatment. N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and also, and also a ctually given a sequence in the Sequence Listing from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oilgonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T7; leukocyte; gene expression profiling; allograft rejection; atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monitoring (the rate of) progression of a disease, e.g. atherosclerosis
or congestive heart failure, comprises diagnostic oligonucleotides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phillips
                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human leukocyte gene expression profiling probe SEQ ID NO 6394
                                                                                                                                                                                                                                                                                                                                          watch 58.3%; Score 14; DB 3; Length 47; Local Similarity 77.3%; Pred. No. 1.2e+04; les 17; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prentice J,
                                                                                                                                                                                                                                                                                                         Sequence 47 BP; 16 A; 13 C; 6 G; 12 T; 0 U; 0 Other;
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T, Johnson F
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Quertermous T,
                                                                                                                                                                                                                                                                                                                                                                                                                            2 ATGCACAGCTGGGGAACAAGAC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 ArĠĆAĆAĊĊrĠTTTCAĊAĠAĊ 46
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08-JUN-2001; 2001US-0296764P.
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Woodward R,
                                                                                                                                                                                                                                                                 present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17, leukocyte, gene expression profiling, allograft rejection; atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
                   rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Altman P, Prentice J, Phillips J; Johnson F;
treatment in an individual. The diseases include cardiac allograft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human leukocyte gene expression profiling probe SEQ ID NO 6784.
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                                                                                                                                        Query Match 58.3%; Score 14; DB 6; Length 50; Best Local Similarity 100.0%; Pred. No. 1.2e+04; Matches 14; Conservative 0; Mismatches 0; Indels
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                                                                                                  Sequence 50 BP; 16 A; 8 C; 19 G; 7 T; 0 U; 0 Other;
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Ly N, Woodward R, Quertermous T,
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                                                                                                                                                                                                                                                                                                                                                                                   BP.
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                                                                                                                                                                                                                                                                                                                                                                                   ABZ06793 standard; DNA; 50
                                                                                                                                                                                                                                    9 GCTGGGGAACAAGA 22
                                                                                                                                                                                                                                                                            31 GCTGGGGAACAAGA 44
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Telerman A,
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Best Local Similarity 88.2
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids in samples, as amplification substrates, to hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP proteins as specifically of hGDMLP proteins as specific biomolecule capture probes for surface-enhanced laser description ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 proteins and in vaccines or for replacement therapy. The polymucleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and sheletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
                                                                                                                                                                                                                                                                                       Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
                                                                                                                                                                                                                                                      Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8469.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 8469; 214pp; English.
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                                                                                                                                             ВЪ.
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30-JAN-2001; 2001WO-US000661.
30-JAN-2001; 2001WO-US000662.
30-JAN-2001; 2001WO-US000663.
30-JAN-2001; 2001WO-US000664.
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2000US-0236359P.
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30-JAN-2001; 2001WO-US000668.
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                                                                                                                                             ABN08477 standard; DNA; 17
                  22
                                                                                                                                                                                                                   (first entry)
                                       GCTGGGGAACAAGA
                    GCTGGGGAACAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                      WO200192524-A2.
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                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid sequences associated with tumor suppression, regression, apoptosis or virus resistance are useful to diagnose and treat viral disease, development of tumor cells and cell degeneration.
The present sequence represents an oligomer used in the screening of the hGDWLP-1 sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         with tumour suppression or regression, apoptosis or virus resistance. invention relates to these sequences or sequences having at least 80% identity to them, and polypeptides encoded by the sequences or polypeptides having 80% identity to the polypeptide sequences. The invention is used to diagnose or treat viral disease or disease characterized by development of tumour cells or cellular degeneration
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                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                              Score 13.8; DB 6; Length 17; Pred. No. 1.3e+04;
                                                                                                                                                                                                                                                                                                             2; Indels
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88.2%; Pred. No. 1.3e+04;
ive 0; Mismatches 2;
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                                                                                                                                                                                        Sequence 17 BP; 6 A; 3 C; 6 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human tumour suppressor sequence #1473.
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                                                                                                                                                                                                                                                                                                                                                                                                                               1 AGCTGGAGACATGACG 17
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The sequences (AAQ53077-Q53136) are used in the invention to detect specific genes without the use of radio-isotopes. Detection is carried out by hybridisation of denatured (ss) sample DNA with a (ss) nucleic acid probe, complementary to the target sequence. Hybridisation occurs on the surface of an electrode or optical fibre and detection is visualised by the addition of an entity that recognises (ds) hybridised DNA and is electrochemically / photochemically active
                                                                                                                                                                                                                                                                                                                       Gene detection; radio-isotopes; target gene; electrode; detection; optical fibre; hybridise; hybridisation; electrochemical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detection method of gene without using radio-isotope - by hybridisation of nucleic acid probe which is single strand having complementary sequence of gene and single strand denatured sample DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe for detecting N-ras gene mutations in the codon at position 61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutated codon, single base mutation, human; acute myeloid leukaemia; tumour; activated ras gene; N-ras; H-ras; K-ras; Bs.
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Indels
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Pred. No. 1.3e+04;
0; Mismatches 2;
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7
Mismatches
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                                                                  1 AGCTGGAGAACATGACG 17
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Best Local Similarity 88.20,
Best Local Similarity 15,
Conservative
                                     8 AGCTGGGGAACAAGACG
                                                                                                                                                                      AAQ53128 standard; DNA; 20
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 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                            AAQ53128;
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                                                                                                                                 RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel polypeptide (I) comprising a sequence (SI) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully defined in the specification, a tragment of at least 8 amino acids fully (SI), 95% deviation from (SI) which are conservative substitutions, and est identity to (SI). A polypeptide of the invention acts as a agonist or antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A pharmaceutical composition of the invention is useful for treating or preventing a disorder associated with decreased expression or activity of hGDMLP-1; usuch as a disorder of heart and/or skeletal muscle function. The present sequence represented a 17-mer nucleotide, used in the invention for scanning the sequence represented in ACN63103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel myosin-like protein-1, useful for treating or preventing disorder associated with decreased expression or activity of human genome-derived myosin-like protein-1 such as disorder of heart and/or skeletal muscle
                                                                                                                                                         Human; 88; probe; myosin-like protein-l; hGDMLP-l;
hGDMLP-l agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
skeletal muscle function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shannon ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.5%; Score 13.8; DB 13; Length 17; 88.2%; Pred. No. 1.3e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 17 BP; 6 A; 3 C; 6 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rank D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, SEQ ID NO 8469; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanzel DK,
                                                                                                                                   Human GDMLP-1 probe SEQ ID NO:8469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001MO-US000665.
2001MO-US000666.
2001MO-US000667.
2001MO-US000669.
2001MO-US000669.
2001MO-US000670.
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2001WO-US000662
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                                                                                                                                                                                                                                                                                                                                                               26-NOV-2003; 2003US-00723361
                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0236359P
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000GB-00024263
                   ACN71567 standard; DNA; 17
                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ji Y, Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PENN S G.
HANZEL D K.
RANK D.
CHEN W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHANNON M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-533378/51.
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Best Local Similarity
                                                                                                                                                                                                                                                                                      US2004137589-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
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GU Y.

(CONYY/)

(JIYY/)

(HANZ/)

(RANK/) (CHEN/)

(SHAN/)

Gu Y,

Function

30-JAN-2001;

0S-FEB-2001; 25-MAY-2001;

30-JAN-2001; 30-JAN-2001; 30-JAN-2001;

04-OCT-2000;

26-MAY-2000; 27-SEP-2000; 21-SEP-2000;

30-JAN-2001;

Homo sapiens

15-JUL-2004

02-DEC-2004

ACN71567;

ACN71567

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Gaps

97WO-SE000839 96SE-00002062

22-MAY-1997; 29-MAY-1996;

WO9745555-A1

04-DEC-1997.

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containing a mutated codon. The method involves: either cleaving a human subject's genomic DNA with a restriction enzyme to produce DNA fragments and treating the fragments to obtain single-stranded DNA molecules or isolating the subject's polyA+ mRNA; contacting the single-stranded DNA molecules or polyA+ mRNA under hybridising conditions with a labelled synthetic DNA molecule, optionally bound to a solid support, comprising 12-20 nucleotides, where the synthetic DNA molecule is 5'-B-Q-D-3' in the case of polyA+ mRNA = 0-9 nucleotides having a sequence complementary to 5'-B-Q-D-3' in the case of polyA+ mRNA = 0-9 nucleotides having a sequence complementary to a sequence in the activated ras gene 5' of the mutated codon, D = 0-12 nucleotides having a sequence complementary to a sequence in the cativated ras gene 5' of the mutated codon, provided that B and D contain a total of at least 9 nucleotides, and Q is complementary to the mutated codon, treating the presence of the labelled synthetic DNA molecule in the detecting the presence of the labelled synthetic DNA molecule in the probation of and has a single base substitution in the first or second nucleotide position so that it encodes an amino acid other than certain the used for the diagnosis of acute myeloid leukaemia conducts. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                          Detection of activated ras gene - using oligo:nucleotide probes to detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.5%; Score 13.8; DB 2; Length 20; 88.2%; Pred. No. 1.3e+04; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probe; N-ras; mutation detection; mismatch binding protein; cancer diagnosis; single strand binding protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 2 A; 7 C; 2 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                            Claim 25; Col 29; 20pp; English
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                                                                                                                 94US-00264425.
                                                                                                                                                   85US-00758104.
                                                                                                                                                                   87US-00081490
92US-00873352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 ACAGCTGGAGAAGA
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                                                                                                                                                                                                                       (UYLE-) RIJKSUNIV LEIDEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15; Conservative
                                                                                                                                                                                                                                                          Van Der Eb AJ, Bos JL;
                                                                                                                                                                                                                                                                                        WPI; 1997-086629/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sest Local Similarity
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                                                                                                                                                                                                                                                                                                                                              mutated codon.
                                                                                                                   23-JUN-1994;
                                                                                                                                                 23-JUL-1985;
                                                                                                                                                                   04-AUG-1987;
21-APR-1992;
                                               US5591582-A.
                                                                                 07-JAN-1997
               Synthetic.
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This sequence represents a probe for the N-ras gene, that can be used in the method of the invention. The method is for for detecting a mutation from a non-mutated sequence of a target polymucleotide (TP) in a sample, by using a mismatch binding protein (MBP), comprises: (a) providing a non-mutated and mutated TP; (b) forming duplex of the non-mutated and contacted single strands of TP in (a); (c) adding a single strand binding continuated single strands of TP in (a); (d) incubating MBP with an activating agent; (e) adding the incubated MBP from (d) to the polymucleotide from (c), so that MBP binds to the duplex formed by one con-mutated and one mutated single strand of TP; and (f) detecting the presence of any MBP bound to TP. The method may be used for early diagnosis of cancer. Binding of MBP to single strands is inhibited by the single strand binding protein. By activating MBP with an activator, before addition to the sample, binding to double strands lacking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                 Method for detecting mutation(s) by mismatch binding protein - useful for separating mutation from non-mutated target polynucleotide in sample,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ras oncogene; probe; point mutation; detection; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 2 A; 7 C; 2 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                   used in early diagnosis of cancer.
                                                                                                                                                                                                                                                                                                  Disclosure; Page 9; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mismatches does not take place
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22
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87US-00081490.
92US-00873352.
94US-00264425.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ras oncogene probe #13
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                                                                                                                                       (PHAA ) PHARMACIA BIOTECH AB
                                                                                                                                                                      Tosu M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 ACAGCTGGGGAACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                     WPI; 1998-130209/12.
                                                                                                                                                                      Goto M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-AUG-1987;
21-APR-1992;
23-JUN-1994;
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                                                                                                                                                                        Hasebe M,
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The present invention describes a method of arraying genome clones. The method comprises: (a) clones of the genomic libraries contained in method comprises: (a) clones of the genomic libraries contained in continuities numbered for discrimination are mixed in each of the multiwell plates; (b) a primer designed based on the chromosome marker contained; a signal corresponding to the marker is detected from the resultant confidence is obscitly the discrimination Nos. of the multiwell plates containing the clones having said marker sequence; (d) the order of the maximum in the specified discrimination Nos. to array the multiwell confidentiation Nos. to are mixed clones of the specified discrimination Nos. to array the multiwell confidentiation Nos. are mixed respectively in each wells of Ingitudinal and lateral directions; (f) the mixed clones are cultured and the capultant cultures are amplified by using the above primer; (g) signals care detected from the amplified products; (h) the clones in the multiwell plates are specified from the amplified products; (h) the clones are cultured and the constituted as the positions on the chromosome and arrayed. The constituted as the positions on the chromosome and arrayed. The constituted is useful for gene analysis. ABL45325 to paresent PCR primers for human chromosome 1936-35 DNA, and ABL45323 to ABL45634 crepresent PCR primers for human chromosome 21q22.1, which are greatly in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
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                Length 20;
                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Human chromosome 1p36-35 PCR primer SEQ ID NO:598
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           57.5%; Score 13.8; DB 2;
88.2%; Pred. No. 1.3e+04;
cive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 16; 528pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RIKA ) RIKAGAKU KENKYUSHO.
                                                                                                                                                     20 acaccrecacadadada
                                                                                                                                                                                                                                                                     ABL43554 standard; DNA; 20
                                                                                                          ACAGCTGGGGAACAAGA
                                                                                                                                                                                                                                                                                                                                                             11-APR-2002 (first entry)
                Query Match
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arraying genome clones.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP2001321190-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR primer; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                  ABL43554;
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                                                                                                                                                                                                                                             AAV73026-V73071 are probes used to detect a single-base mutation in a human ras oncogene. These probes comprise 12-43 nucleotides of formula 5'-B-Q-D-3', Q=3 nucleotides complementary to the mutated codon, and B and D each = 0-20 nucleotides complementary to the ras sequences flanking the mutated codon. The probes are useful for detecting cancers associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probes for detecting ras oncogene point mutations - useful for the diagnosis of cancer associated with single base mutations.
                                                                                                                                  Probes for detecting ras oncogene point mutations - useful for the diagnosis of cancer associated with single base mutations.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.5%; Score 13.8; DB 2; Length 20; 88.2%; Pred. No. 1.3e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ras oncogene; probe; point mutation; detection; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 9 A; 2 C; 7 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV73141 standard; DNA; 20 BP
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87US-00081490.
92US-00873352.
94US-00264425.
                                                                                                                                                                                                       Claim 6; Col 5; 18pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Conservative
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(UYLE-) RIJKSUNIV LEIDEN
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                                          Van Der Eb AJ;
                                                                                                                                                                                                                                                                                                                                                                  with point mutations
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                                                                                     WPI; 1999-059149/05
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23-JUN-1994;
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04-AUG-1987;
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                                          Bos JL,
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Synthetic

ADJ22962;

RESULT 27

ADJ22962

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New antisense oligonucleotide for modulating endothelial lipase expression, for diagnosing, preventing or treating e.g. dyslipidemia, low high density lipoprotein or cardiovascular disorders.
                                                                                                                       Antilipaemic, Cardiovascular, Analgesic, Antianginal; Antisense therapy;
Human, Endothelial Lipase, dyslipidaemia, high density lipoprotein; HDL;
cardiovascular disorder; metabolic syndrome X; ss.
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/note= "This oligonucleotide has a phosphorothioate
backbon and 2- methyoxyethyl (2'-WOE) wings at the 5'
and 3' ends, which are 4 nucleotides in length. Also all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to antisense oligonucleotides (ADJ21603-ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence (ADJ25517), where the antisense oligonucleotide specifically hybridises with and inhibits the expression of EL. The antisense oligonucleotides are useful for modulating the expression of endothelial lipase in cells or tissues to treat diseases associated with EL expression, such as dyslipidaemia, low high density lipoprotein (HDL), cardiovascular disorder or metabolic syndrome X. In addition, the oligonucleotides are used for diagnostics, prophylaxis, or as research reagents or kits.
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                                                                                   Human endothelial lipase antisense oligonucleotide, SEQ ID 1696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.5%; Score 13.8; DB 12; Length 20; 88.2%; Pred. No. 1.3e+04; ive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                  cytidine residues are 5-methylcytidines"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; SEQ ID NO 1696; 1007pp; English.
                                                                                                                                                                                                                                                                                Location/Qualifiers
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modified_base
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                                                                                                                                                                                                                                     Synthetic.
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ADJ23298;
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Best Local (
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                                                                                                                                                                                                                                                       Antilipaemic, Cardiovascular; Analgesic; Antianginal; Antisense therapy; Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL; cardiovascular disorder; metabolic syndrome X; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "This oligonucleotide has a phosphorothioate backbone and 2-'methyoxyethyl (2'-MOE) wings at the 5' and 3' ends, which are 4 nucleotides in length. Also all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to antisense oligonucleotides (ADJ21603-ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence (ADJ25517), where the antisense oligonucleotide specifically hybridises with and inhibits the expression of EL. The antisense oligonucleotides are useful for modulating the expression of endothelial lipase in cells or tissues to treat diseases associated with EL expression, such as dyslipidaemia, low high density lipoprotein (HDL), cardiovascular disorder or metabolic syndrome X. In addition, the oligonucleotides are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         used for diagnostics, prophylaxis, or as research reagents or kits.
                                                                                                                                                                                                                 Human endothelial lipase antisense oligonucleotide, SEQ ID 1360.
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Pred. No. 1.3e+04;
0; Mismatches 2; Indels (
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/mod_base= OTHER
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                                                                                     ADJ22962 standard; DNA; 20 BP.
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illarity 88.2%;
Conservative 0
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Matches 15; Conserv
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modified_base
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(PHAA ) PHARMACIA CORP
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modified_base
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ABN13371
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                                                                                                                                                                                                            /mod_base= OTHER
/note= "This oligonucleotide has a phosphorothicate
backbone and 2-'methyoxyethyl (2'-NOE) wings at the 5'
and 3' ends, which are 4 nucleotides in length. Also all
cytidine residues are 5-methylcytidines"
Antilipaemic, Cardiovascular; Analgesic; Antianginal; Antisense therapy; Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL; cardiovascular disorder; metabolic syndrome X; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to antisense oligonucleotides (ADJ21603-ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence (ADJ25517), where the antisense oligonucleotide specifically hybridises with and inhibits the expression of EL. The antisense oligonucleotides are useful for modulating the expression of endothelial lipase in cells or tissues to treat diseases associated with EL expression, such as dyslipidaemia, low high density lipoprotein (HDL), cardiovascular disorder or metabolic syndrome X. In addition, the oligonucleotides are used for diagnostics, prophylaxis, or as research reagents or kits.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 20 BP; 4 A; 3 C; 11 G; 2 T; 0 U; 0 Other;
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les 15; Conserv
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                                                                                                                                                     Key
modified_base
                                                                                     Homo sapiens.
Synthetic.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antisense oligonucleotide for modulating endothelial lipase expression, for diagnosing, preventing or treating e.g. dyslipidemia, low high density lipoprotein or cardiovascular disorders.
                                                                                                 /mcd_base= OTHER
/note= "This oligonucleotide has a phosphorothioate
backbone and 2-"methyoxyethyl (2'-MOE) wings at the 5'
and 3' ands, which are 4 nucleotides in length. Also all
cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to antisense oligonucleotides (ADJ21603-ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence (ADJ25517), where the antisense oligonucleotide specifically hybridises with and inhibits the expression of EL. The antisense oligonucleotides are useful for modulating the expression of endothelial lipase in cells or tissues to treat diseases associated with EL expression, such as dyslipidaemia, low high density lipoprotein (HDL), cardiovascular disorder or metabolic syndrome X. In addition, the oligonucleotides are used for diagnostics, prophylaxis, or as research reagents or kits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
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Pred. No. 1.3e+04;
0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 5 A; 3 C; 11 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; SEQ ID NO 1929; 1007pp; English.
Location/Qualifiers
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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 can be used as probes to detect, characterise and quantify nucleic acids in samples, as amplification substrates, to protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The proteine sequences encoding having specific deficiency in hGDMLP-1 and secletal muscle disorders. hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.

The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence data for this patent did not form part of the printed that the sequence of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25 BP; 8 A; 6 C; 9 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                            Rank DR,
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2001WO-US000670.
2001US-0266860P.
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2001WO-US000666,
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2001WO-US000663
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nes 15, Conservative
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                                                                                                                                                                                                                                                                                                                                                                 (AEOM-) AEOMICA INC.
                                                                                                        30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
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30-JAN-2001;
30-JAN-2001;
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protein 1 (AGDMLP-1). The protein and polynucleotide sequences of helder protein 1 (AGDMLP-1). The protein and polynucleotide sequences of helder 1 can be used as probes to detect, characterise and quantify helder acids can be used as probes to detect, characterise and quantify helder acids can be used as probes to detect, characterise and quantify helder initial substrates for the recombinant engineering of hCDMLP-1 protein variants having desired phenotypic improvements, and for protein variants having desired phenotypic improvements, and for used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP-1 proteins, as specifically of hGDMLP-1 proteins, as specifically of hGDMLP-1 capture probes for surface-enhanced laser desorption ionisation, as therefore supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The constrained sequence represents an oligomer used in the streaming of the chopy. The present sequence represents an oligomer used in the screening of the hopping-1 sequence of this patent did not form part of the printed to the printed of the sequence of the present invention. N.B. The specification, but was obtained in electronic format directly from MIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
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Pred. No. 1.4e+04;
0; Mismatches 2; Indels
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30-JAN-2001; 2001WO-US000665.
30-JAN-2001; 2001WO-US000666.
30-JAN-2001; 2001WO-US000667.
30-JAN-2001; 2001WO-US000669.
30-JAN-2001; 2001WO-US000669.
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30-JAN-2001; 2001WO-US000663
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Best Local Similarity 88.2
Matches 15; Conservative
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04-OCT-2000;
                                                                 Homo sapiens.
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Indels

Mismatches

WO200192524-A2.

06-DEC-2001

Homo sapiens.

29-MAY-2002

ABN13376;

RESULT 33 ABN13376

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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as
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                                                Score 13.8; DB 6; Length 25; Pred. No. 1.4e+04;
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Seguence 25 BP; 9 A; 5 C; 9 G; 2 T; 0 U; 0 Other;
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30-JAN-2001; 2001WO-US000667.
30-JAN-2001; 2001WO-US000668.
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2001WO-US000670.
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                                                                                                    15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-179446/23.
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                                           Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                            RESULT 34
ABN13373
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                                                                                                                                                                                                   요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify concleic acids in samples, as amplification substrates, to hGDMLP-1 nucleic acids in samples, as amplification substrates, to hGDMLP-1 nucleic acids in samples, as amplification substrates, to protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP-proteins, as specific biomolecule capture probes for surface-enhanced laser description ionisation, as therapeutic supplement in partients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The concentration and skeletal muscle disorders. hGDMLP-1 may be used for diagnosing a clisorders associated with the expression of hGDMLP-1 capture for this patent did not form part of the printed capture for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at figures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
                                                                                                                                                                                                                                                    Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
                                                                                                                                                                                                         Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13368.
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2001WO-US000664.
2001WO-US000664.
2001WO-US000665.
                                                        ABN13376 standard; DNA; 25 BP.
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2000US-0236359P
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30-JAN-2001; 30-JAN-2001; 30-JAN-2001;

30-JAN-2001; 30-JAN-2001; 30-JAN-2001;

30-JAN-2001; 30-JAN-2001;

30-JAN-2001;

30-JAN-2001;

04-OCT-2000;

27-SEP-2000

26-MAY-2000;

Shannon ME;

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RESULT 36
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therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The polymucleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
                                                                                                                                                                                                                                                                                                                                                          Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
                                                                                                                                                                    Gaps
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                                                                                                                                            Score 13.8; DB 6; Length 25;
Pred. No. 1.4e+04;
0; Mismatches 2; Indels
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                                                                                                                         Sequence 25 BP; 8 A; 5 C; 10 G; 2 T; 0 U; 0 Other;
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30-JAN-2001; 2001WO-US000666.
30-JAN-2001; 2001WO-US000667.
30-JAN-2001; 2001WO-US000668.
30-JAN-2001; 2001WO-US000669.
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2001WO-US000663.
2001WO-US000664.
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88.2%;
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Best Local Similarity 88.2
Matches 15; Conservative
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30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                   29-MAY-2002
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27-SEP-2000;
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protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 capture probes for surface-enhanced laser desorption ionisation, as the rapeutic supplement in patients having specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as the rapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The companies engaged with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.

The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present invention. N.B. ChopMLP-1 sequence data for this patent did not form part of the printed constitution in the exemplification of the present directly from WIPO process of the present directly directly directly directly directly directly directly directly directly dire
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2001WO-US000670.
2001US-0266860P.
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Best Local Similarity 88.2
Matches 15; Conservative
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30-JAN-2001;
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-DEC-2001
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us-10-713-137-3.sizlim.rng

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2001WO-US000664
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             30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
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                                                                                                                                                       Ji Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAY-2002
 30-JAN-2001;
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                                                                                                                                                       Gu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABN13374
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used as probes to detect, characterise and quantify nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polymeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as specifically recognise hGDMLP-1 proteins, as specifically recognise hGDMLP-1 proteins, as specific biomolecule and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser describing in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder sapencie with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.

The present sequence represents an oligomer used in the screening of the horseptic and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.

The present data for the exemplification of the present invention. N.B.

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp. wipo.int/pub/published_pot_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                    New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13361.
 Shannon ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.5%; Score 13.8; DB 6; Length 25; 88.2%; Pred. No. 1.4e+04; ive 0; Mismatches 2; Indels
 Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25 BP; 10 A; 5 C; 8 G; 2 T; 0 U; 0 Other;
 Rank DR,
                                                                                                               Disclosure; SEQ ID NO 13369; 214pp; English
Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 AGCTGGGGAACAAGACG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABN13369 standard; DNA; 25 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AGCTGGAGAACATGACG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0234687P,
2000US-0236359P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001WO-US000662.
2001WO-US000662.
2001WO-US000663.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 88.2
Best Local Si Conservative
 Gu Y, Ji Y, Penn SG,
                             WPI; 2002-179446/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200192524-A2.
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27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABN13369;
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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids in samples, as amplification substrates to nucleic acids in samples, as amplification substrates, to hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for cyptessing the proteins. The hGDMLP-1 proteins or polypeptides may be repeated immunospens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP-proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionication, as therapulation in an in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The concentration and skeletal muscle disorders, hGDMLP-1 may be used for diagnosing a clisorders, hGDMLP-1 is localised to chromosome 22.

The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence on the exemplification of the present invention. N.B. Cr The sequence data for this patent did not form part of the printed specification, but was obtained in alectronic format directly from WIPO cat fib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                      Shannon ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25 BP; 8 A; 6 C; 9 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.5%; Score 13.8; DB 6; 88.2%; Pred. No. 1.4e+04;
                                                                                                                                                                                                                                                                                                                                                                                                      Hanzel DK, Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 13361; 214pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                 2001WO-US000668.
2001WO-US000669.
2001WO-US000670.
2001WO-US000665.
2001WO-US000666.
2001WO-US000667.
                                                                                                                 30-JAN-2001; 2001WO-US000668
30-JAN-2001; 2001WO-US00669
30-JAN-2001; 2001WO-US000670
35-FEB-2001; 2001US-0266860P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABN13374 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                          Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-179446/23.
                                                                                                                                                                                                                                                                                                                          (AEOM-) AEOMICA INC.
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Best Local Similarity
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06-DEC-2001

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New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 13366; 214pp; English
                                                                                                                                                                              Hanzel DK,
                               2000US-0207456P.
2000US-0234687P.
2000US-0236359P.
                                                              2001WO-US000661.
2001WO-US000662.
2001WO-US000663.
                                                                                               2001WO-US000665.
                                                                                                     30-JAN-2001; 2001WO-US000666.
                                                                                                                      2001WO-US000668.
                                                                                                                               30-JAN-2001; 2001WO-US000669.
                                                                                      2001WO-US000664
                                                                                                                                     2001WO-US000670
                                                                                                                                              2001US-0266860P
               25-MAY-2001; 2001WO-US016981
                                                      2000GB-00024263
                                                                                                                                                                              Ji Y, Penn SG,
                                                                                                                                                                                              WPI; 2002-179446/23.
                                                                                                                                                              (AEOM-) AEOMICA INC.
                                                                                                                                              05-FEB-2001;
                                                               30-JAN-2001;
                                                                                               30-JAN-2001;
                                                                                                                        30-JAN-2001;
                                                                             30-JAN-2001;
                                                                                       30-JAN-2001;
                                                        04-OCT-2000;
                               26-MAY-2000;
                                               27-SEP-2000;
                                                                                                                                                                              Gu Y,
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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterises and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates to hGDMLP-1 nucleic acids in samples, as amplification substrates to be provided initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be cased as immunoagens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser description indisation, as tharapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The concentration disorders senceding hGDMLP-1 matterlar muscle disorders. hGDMLP-1 is localised to chromosome 22.

The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence date for this patent did not form part of the printed to the concentration the capture of the present invention. N.B. The sequence date for this patent did not form part of the printed to the concentration of the present directly from MIPO and success the production of the present directly from MIPO and success the printed of the printed the concentration of the present directly from MIPO and success the production of the present directly from MIPO and success the production of the present directly from MIPO and success the production of the present directly from MIPO and success the present directly matterly and success the present directly matterly and success the present directly matterly and success the present directly matte

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                                                                     57.5%; Score 13.8; DB 6; Length 25; 88.2%; Pred. No. 1.4e+04; ive 0; Mismatches 2; Indels
                                   Sequence 25 BP; 8 A; 5 C; 10 G; 2 T; 0 U; 0 Other;
at ftp.wipo.int/pub/published_pct_sequence
                                                                                                                                                    8 AGCTGGGGAACAAGACG 24
                                                                                                                                                                              4 AGCTGGAGAACATGACG
                                                                                           Local Similarity 88.2
Les 15, Conservative
                                                                             Query Match
                                                                                                                  Matches
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BP.
                ABN13375 standard; DNA; 25
                                                (first entry)
                                                29-MAY-2002
                               ABN13375;
RESULT 39
        ABN13375
                axyxa
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Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss. Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13367. Hanzel DK, Rank DR, Chen W, Shannon ME; 2001WO-US000664 2001WO-US000665 2001WO-US000666 2001WO-US000667 2001WO-US000669 2001WO-US000670 2000US-0236359P 2000GB-00024263 2001WO-US000662 2001WO-US000663 05-FEB-2001; 2001US-0266860P 25-MAY-2001; 2001WO-US016981 2001WO-US000661 Gu Y, Ji Y, Penn SG, WPI; 2002-179446/23. (AEOM-) AEOMICA INC. WO200192524-A2. 30-JAN-2001; 2 30-JAN-2001; 2 30-JAN-2001; 2 30-JAN-2001; 2 30-JAN-2001; 27-SEP-2000; 04-OCT-2000; 30-JAN-2001; 30-JAN-2001; 30-JAN-2001; Homo sapiens 21-SEP-2000; 06-DEC-2001.

Shannon ME;

Chen W,

Rank DR,

New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser descrption ionization, comprises human myosin-like protein hGDMLP-1.

Disclosure; SEQ ID NO 13367; 214pp; English.

The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 calculated acids can be used as probes to detect, characterise and quantify conclein acids can be used as probes to detect, characterise and quantify provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for capressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as specific blomolecule capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The can skeletal muscle disorders hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart can skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.

The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence data for this patent did not form part of the printed capture in the exemplification of the present invention. N.B. The state of the printed of the ftp.wipo.int/pub/published_pct_sequence

Sequence 25 BP; 8 A; 6 C; 9 G; 2 T; 0 U; 0 Other;

Gaps . 0 57.5%; Score 13.8; DB 6; Length 25; 88.2%; Pred. No. 1.4e+04; Indels 0; Mismatches Query Match Best Local Similarity 88.29 Matches 15; Conservative

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3 AGCTGGAGAACATGACG 19

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The invention describes a dimer of a chimeric recombinant binding domain-
functional group fusion formed via disulfide-bond-bridge and a production
process thereof. The dimer has two times improved adhesion, and
excellently functions on a target. A dimer of chimeric recombinant
binding domain-functional group fusion is provided, wherein an extended
c binding domain-functional group fusion is provided, wherein an extended
c mino acid sequence (Ext) which is extended from the binding domain (B)
to the function group (F) fuses the binding domain (B)
c proup (F); the extended amino acid sequence (Ext) contains cysteine
without an inner chain pair and forms disulfide-bond-bridge when the
cysteine is oxidised, and a flexible amino acid sequence (Flx) is
c contained between the last cysteine and the functional group (F), and
c consists of flexible amino acid sequences of GASQEND, so that it can
decrease steric hindrance between the functional group when the chimeric
recombinant binding domain(B) functional group (F) fusion forms the
dimer. This sequence represents a primer associated with the chimeric
recombinant binding domain-functional group fusion of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dimer of chimeric recombinant binding domain-functional group fusion formed via disulfide-bond-bridge and production process thereof.
                                                                                                                                                               dimer; chimeric recombinant binding domain-functional group fusion; steric hindrance; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Won JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.5%; Score 13.8; DB 12; Length 25; 88.2%; Pred. No. 1.4e+04;
                                                                                                                                 Binding domain-functional group fusion related pRK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Song JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25 BP; 1 A; 10 C; 9 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kim YJ, Kwon HW, Lee YC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 25; 65pp; Korean.
                BP.
                                                                                                                                                                                                                                                                                                                                                        30-JUN-2003; 2003KR-00043599
                                                                                                                                                                                                                                                                                                                                                                                           29-JUN-2002; 2002KR-00037770
ADQ80648/c
ID ADQ80648 standard; DNA; 25
                                                                                            (first entry)
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Best Local Similarity 88.2
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Choi SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHOE/) CHOE M H.
                                                                                                                                                                                                                                                                        KR2004004095-A.
                                                                                                                                                                                                                                 Unidentified
                                                                                            09-SEP-2004
                                                                                                                                                                                                                                                                                                               13-JAN-2004
                                                       ADQ80648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Choe MH,
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0; Gaps

Indels

0; Mismatches

4 GCACAGCTGGGGAACAA 20

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GCGCGCTGGGGACAA

Search completed: December 13, 2005, 13:34:17 Job time : 371.5 secs

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Pasha, A.Q. and Ahsan, A.
Method of detecting predisposition to high altitude pulmonary edema
Patent: WO 2005047540-A 3 26-MAY-2005;
Council of Scientific and Industrial Research (IN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAT 19-JAN-2005
AR167144 Sequence
BD088354 A method
I02471 Sequence 3
AB067911 Synthetic
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                             AB067911 Syntheric
CQ628621 Sequence
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CQ628625 Sequence
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CQ628629 Sequence
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AR469680 Sequence
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AR469690 Sequence
AR469691 Sequence
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/organism="synthetic construct"
/orl_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="Synthetic Oligonucleotide"
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100.0%; Pred. No. 1.3;
iive 0; Mismatches 0;
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Sequence 35 from Patent WO2005000888.
CQ979281.1 GI:57976534
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                               AB067911
CQ628621
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CQ628626
CQ628627
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CQ896911 Sequence
AX58101 Sequence
AX642888 Sequence
CQ878645 Sequence
CQ890107 Sequence
AX487198 Sequence
EZ6387 Neuralized
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CQ623729 Sequence
AR464792 Sequence
AX673028 Sequence
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CQ979281 Sequence
AR071012 Sequence
AR290262 Sequence
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35 Surface p
                                                                          December 13, 2005, 12:48:14 ; Search time 1116.5 Seconds (without alignments) 1221.892 Million cell updates/sec
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              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                        5883141 seqs, 28421725653 residues
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Maximum Match 100%
Listing first 45 summaries
                                                        nucleic search, using sw model
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seq length: 50
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Minimum DB Maximum DB

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Searched:

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Butz,K., Crnkovic-Mertens,I. and Hoppe-Seyler,F.D.
Livin-specific siRNAs for the treatment of therapy-resistant tumors
Patent: EP 1469070-A 1 20-OCT-2004,
Butsches Krebsforschungszentrum Stiftung des oeffentliche n Rechts
(DE)
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LIVIN-SPECIFIC siRNAS FOR THE TREATMENT OF THERAPY-RESISTANT TUMORS
Patent: WO 2004091388-A 1 28-OCT-2004;
Deutsches Krebsforschungszentrum Stiftung des oeffentliche n Rechts
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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93.8%; Pred. No. 7.7e+04;
tive 0; Mismatches 1;
                                                               ch 60.8%; Score 14.6; DB 6; Similarity 73.9%; Pred. No. 5.8e+04; 17; Conservative 1; Mismatches 5;
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Sequence 1 from Patent WO2004091388.
CQ896981. GI:55581823

    .19
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aguence 1 from Patent EP1469070.
CQ890345
CQ890345.1 GI:55163328
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CQ896981/c
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CQ890345/c
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                                                                                                                                    /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="forward primer for amplifying beta-actin promoter containing intron 1"
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Unclassified.
In (bases 1 to 38)
S (Cho,J.Myung., Choi,D.Young., Kim,C.Hyung., So,H.Seob., Yang,J.Young., Kim,J.Ho.
HCV diagnostic agents
HCV diagnostic agents
Location/Qualifiers
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Cohen,D., Chumakov,I. and Blumenfeld,M.
Biallelic markers for use in constructing a high density disequilibrium map of the human genome
Patent: US 6537751-A 1997 25-MAR-2003;
FRX;
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                                Estes, S.D. and Zhang, W.
Novel Beta-actin and RPS21 promoters and uses thereof
Patent: WO 2005000888-A 35 06-JAN-2005;
Genzyme Corporation (US)
Location/Qualifiers
                                                                                                                                                                                                                                                     Query Match 65.0%; Score 15.6; DB 6; Length 26; Best Local Similarity 81.8%; Pred. No. 1.9e+04; Matches 18; Conservative 0; Mismatches 4; Indels
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     other sequences; artificial sequences
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/mol_type="unassigned DNA"
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Sequence 13 from patent US 5910405.
AR071012
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AR290262
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                                     PAT 04-0CT-2004
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Human p53 splice variant displaying differential transcriptional
activity
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Novel human p53 splice variant displaying differential
transcriptional activity
Patent: WO04008548A 17 07-OCT-2004;
Deppert, WO1fgang Willi (DE)
Location/Qualifiers
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Pred. No. 9.6e+04;
0; Mismatches 3;
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/note="Primer EllR"
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/note="primer BllR"
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Sequence 17 from Patent WO2004085468.
CQ890107
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synthetic construct
other sequences; artificial sequences.
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other sequences; artificial sequences.
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Deppert, Wolfgang Willi (DE)
Location/Qualifiers
                                       CQ878645 21 bp
Sequence 17 from Patent EP1462521.
CQ878645 GI:53791103
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Best Local Similarity 84.2%;
Matches 16; Conservative
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Best Local Similarity 84.2
Matches 16; Conservative
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           RESULT 9
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Method for the preferential nucleic acid synthesis reaction of one or more selected regions of one or more target nucleic acids
Patent: WO 02086155-A 7 31-0CT-2002;
LION Bioscience AG (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Musinae; Mus.
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Method of blocking amplification of selected sequences
Patent: BP 1253205-A 7 30-OCT-2002;
LION Blocsience AG (DE)
Location/Qualifiers
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93.8%; Pred. No. 7.7e+04;
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60.0%; Score 14.4; DB 6;
Best Local Similarity 75.0%; Pred. No. 7.5e+04;
Matches 18; Conservative 0; Mismatches 6;

    .30
    forganism="synthetic construct"
|mol type="unassigned DNA"
|db_xref="taxon:32630"

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                                                                                                                                                                                                                                                                                  other sequences; artificial sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="unassigned DNA"
/db_xref="taxon:10090"
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Squence 7 from Patent W002086155.
AX642888 GI:28475108
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/organism="Mus musculus"
                                                                                                                                                                     AX588101 30 bp
Sequence 7 from Patent EP1253205.
AX588101 GI:27899755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GATGCACAGCTGGGGAACAAGACG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATGCACGGAGGGAGGAAGAGG 29
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synthetic construct
                                                           6 ACAGCTGGGGAACAAG
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           Best Local Similarity 93.8 Matches 15; Conservative
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AX642888
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AX588101
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FEATURES

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BD082235.1 GI:22627845

$ DP082235.1 GI:22627845

$ Synthetic construct

synthetic construct

time of the sequences; artificial sequences.

Chatwal, G.S. and Hammerschmidt, S.

Surface protein (SPBA protein) of streptococcus pneumoniae, deleted

derivatives, expression system for said proteins and vaccine system

with said proteins

AL Patent: JP 2001524073-A 12 27-NOV-2001;

RESELLSCHAFF FUR BIOTECHNOLOGISCHE FORSCHUNG MBH

PR 20-MAR-1998 JP 1998538137

PR 30-MAR-1999 DE 1998538137

PR 30-MAR-1999 DE 1970833.7

PR CURNIA, SYRN HAWMERSCHMIDT

CC Strandedness: Single;

CC Topology: Linear;

FH Key

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CC Topology: Lineari,

FH Key

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FH Key
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Chhatwal, G.S. and Hammerschmidt, S.
Chhatwal, G.S. and Hammerschmidt, S.
SURFACE PROTEIN (SPEA PROTEIN) OF STREPTOCOCCUS PNEUMONIAE, DELETED SURFACE PROTEIN SEATEM FOR SAID PROTEINS AND VACCINE SYSTEM WITH SAID PROTEINS
PALENT: WO 9819450-A 13 11-SEP-1998;
BIOTECHNOLOG FORSCHUNG GMBH (DE); CHHATWAL GURSHARAN SINGH (DE)
LOCATION/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Surface protein (SP8A protein) of streptococcus pneumoniae, deleted derivatives, expression system for said proteins and vaccine system BD082235
                                      PAT 21-JAN-2000
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58.3%; Score 14; DB 6; Length 37;

Best Local Similarity 77.3%; Pred. No. 1.2e+05;

Matches 17; Conservative 0; Mismatches 5; Indels
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77.3%; Pred. No. 1.2e+05;
iive 0; Mismatches 5;

    .37
    forganism="synthetic construct"
|mol type="genomic DNA"
|db_xref="taxon:32630"

                                        DNA
                                                                                                                                                                                                                                                                                                                                                                                       /organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
                                37 bp
Sequence 13 from Patent W09839450.
A86551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 GATCCACAGGCTGGAACAAGA 33
                                                                                                                                                              unidentified unclassified sequences.
                                                                                                  A86551.1 GI:6735149
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BD082235
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Sunidentified
unclassified.

I (bases 1 to 23)

Motcomi, M., Hiddeo, N., Mitsuhiro, Y. and Hideyuki, S.

I (bases 1 to 23)

Motcomi, M., Hiddeo, N., Mitsuhiro, Y. and Hideyuki, S.

Betent: JP 1999137257-A 14 25-MAY-1999;

SUMITOMO ELECTRIC IND LTD
OS Unidentified

N JP 1999137257-A/14

PR 14-NOV-1997 JP 1997313211

PR MOTOMI NAKADA, HIDEO NAKAMURA, MITSUHIRO YOSHIDA, HIDEYUKI SAYA

PC CIZNIS/09, CIZRI:91), (CIZPZI/02, CIZRI:09), CIZNIS/00, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E26387 linear PAT 18-JUN-2001 Neuralized protein, polynucleotide encoding said protein and antibody recognizing said protein.
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Candida albicans
Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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                                                                                                    Roemer, T., Jiang, B., Boone, C., Bussey, H. and Ohlsen, K.L. Gene disruption methodologies for drug target discovery Patent: WO 02053728-A 4498 11-JUL-2002; Elitra Pharmaccuticals, Inc. (US) Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                   Length 22;
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/organism='Unidentified'
Location/Qualifiers
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Pred. No. 9.6e+04;
0; Mismatches 3;
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                                                                                                                                                                                                                               /organism="Candida albicans"
/mol_type="unassigned DNA"
/db_xref="taxon:5476"

    .23
    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"

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Matches 16; Conservative (
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PAT 27-MAR-2003
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          PAT 20-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Telerman, A., Amson, R. and Tuijnder, M. Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as
                                                                                                                                                                                  Polymuclectide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle patent: US 6686188-A 8469 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo.
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88.2%; Pred. No. 1.5e+05;
iive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                      57.5%; Score 13.8; DB 6; Length 17; 88.2%; Pred. No. 1.5e+05; ive 0; Mismatches 2; Indels
          linear
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17 bp DNA
Sequence 8469 from patent US 6686188.
AR464792.1 GI:42699849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent: WO 03004526-A 1473 16-JAN-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AX673028 17 bp DNA Sequence 1473 from Patent WO03004526. AX673028

    .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Sequence 5 from patent US 6284463.
AR167144 GI:16243619
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Best Local Similarity 88.2
Matches 15; Conservative
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Shannon,M.E.
                                                                                                                                                                                                                                     Unknown:
Unclassified.

1 (bases 1 to 47)

Cohen,D., Chumakov,I. and Blumenfeld,M.

Biallelic markers for use in constructing a high density disequilibrium map of the human genome
Patent: US 6537751-A 1898 25-MAR-2003;
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Aeomica, Inc. (US)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 14; DB 6; Length 47;
pred. No. 1.2e+05;
1; Mismatches 1; Indels
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Sequence 1898 from patent US 6537751.
AR290163
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/organism="unknown"
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Best Local Similarity 87.5%;
Matches 14; Conservative 1
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RESULT 16 CQ623729

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RESULT 17 AR464792

Matches

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Length 20; 2; Indels

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AB067911 20 bp DNA linear SYN 21-MAY-2003
Synthetic construct DNA, reverse primer for human STS sts-F19245 at
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                                         1 (bases 1 to 20)
Bos,J.L. and Van der Eb,A.J.
Probes and methods for detecting activated ras oncogenes
patent: US 4871838-A 3 03-OCT-1989;
                                                                                                      The Board of Rijks Universiteit Leiden; Leiden;
                                                                                                                                                                                                                             57.5%; Score 13.8; DB 6;
88.2%; Pred. No. 1.5e+05;
live 0; Mismatches 2;
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                                                                                                                                     Location/Qualifiers
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AB067911.1 GI:15128715
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Best Local Similarity 88.2
Matches 15; Conservative
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JP 2001321190-A/598
20-NOV-2001
12-NAR-2001
EIICHI SOEDA
CI2N15/09,CI2N15/09,CI2M1/00,CI2Q1/68,G01N33/53,G01N33/566,
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Patent: JP 2001321190-A 598 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
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Location/Qualifiers
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synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 20)
                                              1 (bases 1 to 20)
Hasebb,M., Goto,M. and Tosu,M.
Method for detection of mutations
Patent: US 6284463-A 5 04-SEP-2001;
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A method of arraying genome clone.
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Matches 15; Conservative
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Direct Submission
Submitted (04-AUG-2001) Akira Horii, Tohoku University School of Submitted (04-AUG-2001) Akira Horii, Tohoku University School of Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai, Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp, Tel:81-22-717-8047)
Location/Qualifiers
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lo xref="taxon:32630"
1. .20
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Gaps

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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PAT 02-FEB-2004
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                               Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
Myosin-like gene expressed in human heart and muscle
Patent: WO 0192524-A 13363 06-DEC-2001;
Aeomica, Inc. (US)
Location/Qualifiers
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Myosin-like gene expressed in human heart and muscle
Patent: WO 0192524-A 13364 06-DEC-2001;
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llarity 88.2%; Pred. No. 1.5e+05;
Conservative 0; Mismatches 2;
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Sequence 13365 from Patent W00192524.
CQ628625 GI:41678843
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Sequence 13364 from Patent WO0192524.
CQ628624
                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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/db_xref="taxon:9606"

    .25
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Location/Qualifiers
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Best Local Similarity 88.2
Matches 15; Conservative
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                                                                               Hominidae; Homo.
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CQ628624
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CQ628625
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  PAT 02-FEB-2004
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Myosin-like gene expressed in human heart and muscle
Patent: WO 0192524-A 13362 06-DEC-2001;
                                                                                                                                                                                                                      Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
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Acomica, Inc. (US)
Location/Qualifiers
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Sequence 13362 from Patent WO0192524.
CQ628622
CQ628621 25 bp DN Sequence 13361 from Patent WO0192524.

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Location/Qualifiers
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Myosin-like gene expressed in human heart and muscle
Patent: WO 0192524-A 13369 06-DEC-2001;
Aeomica. Inc. (US)
Location/Qualifiers
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Shannon,M.E.
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Patent: WO 0192524-A 13368 06-DEC-2001;
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88.2%; Pred. No. 1.5e+05;
iive 0; Mismatches 2;
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Sequence 13369 from Patent WO0192524.
CQ628629
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Myosin-like gene expressed in human heart and muscle
Patent: WO 0192524-A 13367 06-DEC-2001;
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                  Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
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Myosin-like gene expressed in human heart and muscle
Patent: WO 0192524-A 13366 06-DEC-2001;
                                              Myosin-like gene expressed in human heart and muscle Patent: WO 0192524-A 13365 06-DEC-2001;
Acomica, Inc. (US)
Location/Qualifiers
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Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2;
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Sequence 13367 from Patent WO0192524.
CQ628627
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Location/Qualifiers
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                                                                                                                                                                                                         Unclassified.

1 (bases 1 to 25)

1 (bases 1 to 25)

Shannon, M. E.

Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle patent: US 668188-A 13363 03-FEB-2004;

Amersham PLC; Buckinghamshire;

GBX;
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Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
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Sequence 13364 from patent US 6686188.
AR469687
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Sequence 13363 from patent US 6686188.
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/organism="unknown"
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8 AGCTGGGGAACAAGACG 24
               8 AGCTGGAGAACATGACG
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Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
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Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
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                                          Query Match 57.5%; Score 13.8; DB 6; Length 25; Best Local Similarity 88.2%; Pred. No. 1.5e+05; Matches 15; Conservative 0; Mismatches 2; Indels
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AR469684
AR469684 GI:42704741
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/organism="unknown"
/mol_type="genomic DNA"
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/organism="unknown"
/wol_type="genomic DNA"
/db_xref="taxon:9606"
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Gu.Y., Ji.Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
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Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
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Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
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88.2%; Pred. No. 1.5e+05;
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88.2%; Pred. No. 1.5e+05;
ative 0; Mismatches 2;
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Sequence 13369 from patent US 6686188.
AR469692
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/organism="unknown"
/mol_type="genomic DNA"
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Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle patent: US 6686188-A 13366 03-FEB-2004;
Amersham PLC; Buckinghamshire;
GBX;
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1 (bases 1 to 25)

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1 (Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 57.5%; Score 13.8; DB 6; Best Local Similarity 88.2%; Pred. No. 1.5e+05; Matches 15; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2;
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       25 bp DNA Sequence 13365 from patent US 6686188. AR469688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AR469689 25 bp DNA
Sequence 13366 from patent US 6686188.
AR469689 1 GI:42704746
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Location/Qualifiers
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Amersham PLC; Buckinghamshire; GBX;
                                         source
                          FEATURES
                                                                         ORIGIN
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Query Match 57.5%; Score 13.8; DB 6; Length 25; Best Local Similarity 88.2%; Pred. No. 1.5e+05; Matches 15; Conservative 0; Mismatches 2; Indels ઠે

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Search completed: December 13, 2005, 14:11:40 Job time : 1118.5 secs Q

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834656, 947795, 1574497,

Sequence Sequence Sequence 1

Sequence 394642, Sequence 394667, Sequence 472467, Sequence 703352,

28077, 1 28079, 1

Sequence Sequence Sequence Sequence Sequence Sequence

28074,

Sequence Sequence Sequence Sequence

Sequence Sequence

on:

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Length 19;
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US-11-101-244-3949795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
US-11-083-784-947800
; Sequence 947800, Application US/11083784
; Publication No. US2050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
. APPLICANT: Leake, Devin
                                                                                                                                                                                                                                                                                                                                              Sequence 947800, Application US/11101244
Publication No. US20050246794A1
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Best Local Similarity 78.9
Matches 15; Conservative
TYPE: RNA
CORGANISM: Homo sapiens
US-11-101-244-947800
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Sequence 947800,
Sequence 947800,
Sequence 386342,
Sequence 386342,
Sequence 17050, A
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332886,
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248753,
287598,
341923,
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882569,
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                                                                              December 13, 2005, 13:34:24 ; Search time 214.5 Seconds (without alignments) 41.830 Million cell updates/sec
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US-11-083-784-947800
US-11-083-784-36342
US-11-083-784-36342
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US-11-083-784-17174
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                                                                                                                                                                                                                 3392430 seqs, 186927314 residues
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Maximum Match 100%
Listing first 45 summaries
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APPLICANT: Barany, Francis
APPLICANT: Turner, Daniel
APPLICANT: Turner, Daniel
APPLICANT: Pingla, Maneesh
APPLICANT: Pingla, Maneesh
APPLICANT: Pinglas, Hannesh
APPLICANT: Pinglas, Hannesh
TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
FILE REFERENCE: 19603/4121 (CRF D-2995-02)
CURRENT APPLICATION NUMBER: US 60/502/731
PRIOR PILLING DATE: 2003-09-12
NUMBER OF SEQ ID NOS: 38895
SOFTWARE: PatentIn version 3.3
SEQ ID NO 11050
LENGTH: 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 19;
                                      APPLICANT: Scaring, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFRENCE: 1349908
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
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PRIOR APPLICATION NUMBER: 60/502,050
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PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: PROPRIETATY
SEQ ID NO 386342
LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 60.0%; Score 14.4; DB 9; Best Local Similarity 87.5%; Pred. No. 5.2e+02; Matches 14; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: Oligonucleotide probe US-10-939-294A-17050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 17050, Application US/10939294A; Publication No. US20050266417A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 647873, Application US/11101244; Publication No. US20050246794A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CAGCGGAGTGATGGCAAGC 19
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APPLICANT: Khvorova, Anastasia
APPLICANT: Reyrolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
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US-10-939-294A-17050
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5.5-10-24-36
## APPLICANT: Scaringe, Stephen
| TITLE OF INVENTION: Functional and Hyperfunctional siRNA |
| FILE REFERENCE: 13499US |
| CURRENT APPLICATION NUMBER: US/11/083,784 |
| CURRENT FILING DATE: 2005-03-18 |
| PRIOR FILING DATE: 2003-11-14 |
| PRIOR FILING DATE: 2003-11-14 |
| PRIOR FILING DATE: 2003-09-10 |
| PRIOR PILING DATE: 2003-09-10 |
| PRIOR FILING DATE: 2003-09-10 |
| PRIOR APPLICATION NUMBER: 60/426,137 |
| PRIOR FILING DATE: 2002-11-14 |
| NUMBER OF SEQ ID NOS: 1591911 |
| SEQ ID NO 947800 |
| LENGTH: 19
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60.0%; Score 14.4; DB 8;
Best Local Similarity 87.5%; Pred. No. 5.2e+02;
Matches 14; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15.8; DB 9;
Pred. No. 1.2e+02;
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Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Rhyorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGACUGAUGGCAAGUACGA 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 78.9%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: RNA
CORGANISM: Homo sapiens
US-11-083-784-947800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: Homo sapiens US-11-101-244-386342
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US-11-083-784-386342
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LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bharmacon, Inc.
APPLICANT: Revnoids, Angela
APPLICANT: Revnoids, Angela
APPLICANT: Revnoids, Angela
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NOS 812569
TRINGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                       Length 19;
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR PELING DATE: 2005-04-07
PRIOR PELING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 882569
LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                         Score 13.4; DB 8;
Pred. No. 1.5e+03;
0; Mismatches 1;
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Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 882569, Application US/11083784; Publication No. US20050245475A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              55.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 AGTAATGGCAAGCAC 5
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Best Local Similarity 93.33
Marches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 55.8
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA
CORGANISM: Homo sapiens
US-11-083-784-882569
                                                                                                                                                                                                                                                                                                          TYPE: RNA
CORGANISM: Homo sapiens
US-11-101-244-882569
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US-11-101-244-248753
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US-11-083-784-647873

US-11-083-784-647873

Sequence 647873, Application US/11083784

PUDLICATION NO. US20050245475A1

GENERAL INFORMATION

APPLICANT: Beynolds, Angela

APPLICANT: Revorova, Anastasia

APPLICANT: Responds, Angela

APPLICANT: Leake, Devin

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REPREMENT Searinge, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE SPERIES 2003-18

CURRENT APPLICATION NUMBER: US/10/714,333

PRIOR FILING DATE: 2003-10-10

PRIOR FILING DATE: 2003-10-10

PRIOR FILING DATE: 2003-10-10

PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

LENGTH: 197873

LENGTH: 197873
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                                                                                                                                                                                                                                                                                                                                                                            Length 19;
        APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2002-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                              Score 13.8; DB 8; Length 1
Pred. No. 9.7e+02;
1; Mismatches 2; Indels
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Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens US-11-083-784-647873
                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-11-101-244-647873
                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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APPLICANT:
APPLICANT:
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Best Local 8
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Sequence 426653, Application US/11101244
Publication No. US2O80246794A1
GENERAL INFORMATION:
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Beake, Devin
APPLICANT: Beake, Devin
APPLICANT: Brashall, William
APPLICANT: Booling, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2005-04-07
PRIOR FILING DATE: 2005-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 426653
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 19;
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                                APPLICANT: Grandler, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REPERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR PLILING DATE: 2005-04-07
PRIOR PLILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PLILING DATE: 2002-011-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
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Pred. No. 1.8e+03;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.0%; Score 13.2; DB 8; 72.2%; Pred. No. 1.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
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Publication No. US20050246794A1
GENERAL INFORMATION:
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APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.0%;
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Best Local Similarity 77.8
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-11-101-244-341923
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US-11-101-244-426653
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i Sequence 287598, Application US/11101244

i Sequence 287598, Application US/11101244

i Sequence 287598, Application US/11101244

i GENERAL INFORMATION:

i APPLICANT: Revorova, Anastasia

i APPLICANT: Revorova, Anastasia

i APPLICANT: Revorova, Manstasia

i APPLICANT: Revorova, Manstasia

i APPLICANT: Revorova, Manstasia

i APPLICANT: Revorova, Manstasia

i APPLICANT: Revorova, Milliam

i APPLICANT: Scaringe, Stephen

i TITLE OF INVENTION: Functional and Hyperfunctional siRNA

i TITLE OF INVENTION: Functional and Hyperfunctional siRNA

i TITLE OF INVENTION: Punctional and Hyperfunctional siRNA

i TITLE OF INVENTION WIMBER: 60/502,050

PRIOR PILING DATE: 2005-04-07

i PRIOR PILING DATE: 2003-09-10

i PRIOR FILING DATE: 2002-11-14

i NUMBER OF SEQ ID NOS: 1591911

i SOTWARE: Proprietary

i ENGTH: 19

i WUDE: DATE: DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 19;
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 248753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
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Pred. No. 1.8e+03;
1; Mismatches 3;
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US-11-101-244-341923
is Sequence 341923, Application US/11101244
is Publication No. US20050246794A1
is GENERAL INFORMATION:
is APPLICANT: Dharmacon, Inc.
is APPLICANT: Khororova, Anastasia
is APPLICANT: Reynolds, Angela
is APPLICANT: Leake, Devin
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Best Local Similarity 77.8%;
Matches 14; Conservative
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Best Local Similarity 72.2
Matches 13; Conservative
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US-11-101-244-248753
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US-11-101-244-287598
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; Sequence 341923, Application US/11083784
; Publication No. US2OSO0245475A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynold, Angela
; APPLICANT: Reynold, Angela
; APPLICANT: Respond, Angela
; APPLICANT: Beake, Devin
; APPLICANT: Beake, Devin
; APPLICANT: Scaringe, Stephen
; TITLE OF INVERTION: Functional and Hyperfunctional siRNA
; TITLE OF INVERTION: Functional and Hyperfunctional siRNA
; TITLE OF INVERTION NUMBER: US/11/083,784
; CURRENT APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-09-10
; PRIOR PLING DATE: 2003-09-10
; PRIOR PLING DATE: 2003-09-10
; RRIOR PLING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; LENGTH: 10
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Pred. No. 1.8e+03;
2; Mismatches 3; Indels
                   APPLICANT: Scaringe, Stephen
TITLE OF INVEXTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 1349908
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
FRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
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Best Local Similarity 72.2%;
Matches 13; Conservative
APPLICANT: Marshall, William
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Matches 13; Conservative
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CRGANISM: Homo sapiens
US-11-083-784-287598
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ORGANISM: Homo sapiens
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US-11-083-784-426653
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; Sequence 248753, Application US/11083784
; Publication No. US20550245475A1
; GRNERAL INFORMATION:
APPLICANT: Marchall
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Respect Carringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFRENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 06/502,050
PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-10-16
; PRIOR FILING DATE: 2003-10-16
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-11-14
; RIOR APPLICATION NUMBER: 60/426,137
; RIOR APPLICATION NUMBER: 60/426,137
; ROPPHER OF SEQ ID NOS: 1591911
                                                                                                                                                                                                                                                                                                                                                                                                           Length 19;
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APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REPERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR PLICATION NUMBER: 60/502,050
PRIOR PLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 770754
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Pred. No. 1.8e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GCGGAGTGATGGCAAGCA 20
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APPLICANT: Khvorcva, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
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Best Local Similarity 77.8°
Matches 14; Conservative
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Best Local Similarity 77.8<sup>†</sup>
Matches 14; Conservative
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CORGANISM: Homo sapiens
US-11-083-784-248753
                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-11-101-244-770754
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LENGTH: 19
                                                                                                                                                                                                                                                                                                                   TYPE: RNA
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Query Match
Best Local Similarity 83.34
Matches 15; Conservative
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Best Local Similarity
Matches 11; Conserv
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US-11-083-784-770754

i Sequence 770754, Application US/11083784

j Publication No. US20550245475A1

i GENERAL INFORMATION:

j APPLICANT: Dharmacon, Inc.

j APPLICANT: Reynolds, Ansetasia

j APPLICANT: Reynolds, Ansetasia

j APPLICANT: Reynolds, Angela

j APPLICANT: Respination William

j APPLICANT: Marshall, William

j APPLICANT: Ascaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 1349908 R. US/11/083,784

CURRENT APPLICATION NUMBER: US/10/714,333

PRIOR APPLICATION NUMBER: G0/502,050

PRIOR APPLICATION NUMBER: G0/426,137

PRIOR FILING DATE: 2003-11-14

SPRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SSEQ ID NO 770754
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APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 1349908
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT APPLICATION NUMBER: US/11/044,333
PRIOR PLILING DATE: 2003-11-14
PRIOR PLILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 426653
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.0%; Score 13.2; DB 9; Length 19; 77.8%; Pred. No. 1.8e+03;
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Pred. No. 1.8e+03;
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US-10-939-294A-17174
; Sequence 17174, Application US/10939294A
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Best Local Similarity 77.8%;
Matches 14; Conservative
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Best Local Similarity 77.8
Matches 14, Conservative
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; ORGANISM: Homo sapiens
US-11-083-784-770754
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Barancis
APPLICANT: Dariel
APPLICANT: Dariel
APPLICANT: Pingle, Manesh
APPLICANTION: Whethods for identifying target nucleic acid molecules
FILE REFERENCE: 19603/4121 (CRF D-2995-02)
CURRENT APPLICATION NUMBER: US/10/939,294A
FILE REFERENCE: 19603/4121 (CRF D-2995-02)
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-12
NUMBER OF SEQ ID NOS: 38895
SOFTWARE: Patentin version 3.3
SEQ ID NO 11174
LENGTH: 32
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APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Barishall, William
APPLICANT: Scaringe, Stephen and Hyperfunctional siRNA
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT APPLICATION NUMBER: 005-04-07
PRIOR FILING DATE: 2005-04-07
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 332886
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Pred. No. 2.2e+03;
2; Mismatches 0; Indels
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; Sequence 32886, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
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APPLICANT: Brown, Eugene
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATIN
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION UNDMER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 21
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Publication No. US20050266409A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATINTILE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION UNDERF: US/10/770,726
CURRENT APPLICATION UNDERF: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
SEQ ID NO 27534
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100.0%; Pred. No. 2.3e+03;
:ive 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/10/770,726 CURRENT FILING DATE: 2004-02-04 NUMBER OF SEQ ID NOS: 48640 SOFTWARE: PATENTIN VERSION 3.2
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GENERAL INFORMATION:
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Best Local Similarity 84.6'
***rhes 11; Conservative
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Best Local Similarity 84.6
Matches 11; Conservative
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Best Local Similarity 100.
Matches 13; Conservative
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; ORGANISM: RNAi
US-10-770-726-27534
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US-10-770-726-27533
                                                                                                                                                           SEQ ID NO 27036
LENGTH: 21
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US-10-726-27036

US-10-770-126-27036

SQUENCE 27036, Application US/10770726

Publication No. US20050266409A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Liu, Wei

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING

TITLE OF INVENTION: CANCERS

FILE REFERENCE: AM101079 (031896-010000)
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Pred. No. 2.3e+03;
0; Mismatches 0; Indels
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100.0%; Pre
               Khvorova, Anastasia
Reynolds, Angela
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4 GAGUGAUGGCAAG 16
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Best Local Similarity 100.
Matches 13; Conservative
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Matches 11; Conservative
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US-11-083-784-332886
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US-10-770-726-27035
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APPLICANT:
APPLICANT:
APPLICANT:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING, TITLE OF INVENTION: CANCERS, FILE REFERENCE: AMIO1079 (031896-010000); CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
LENGTH: 21
TYPE: ....
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| Publication No. US20050266409A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Wyeth
| APPLICANT: Liu, Wei
| APPLICANT: Liu
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| Publication No. US20050266409A1
| CRNERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Wyeth
| APPLICANT: Brown, Eugene
| APPLICANT: Liu, Wei
| TITLE OF INVENTION: CANCERS
| TITLE OF INVENTION: CANCERS
| FILE REFERENCE: AMI01079 (031896-010000)
| TITLE OF INVENTION: CANCERS
| FILE REFERENCE: AMI01079 (131896-010000)
| CURRENT RELING DATE: 2004-02-04
| NUMBER OF SEQ ID NOS: 48640
| SOFTWARE: Parentin version 3.2
| SEQ ID NO 27990
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Pred. No. 2.3e+03;
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100.0%; Pred. No. ...
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Best Local Similarity 100.
Matches 13; Conservative
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US-10-770-726-27539
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US-10-770-726-27989
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US-10-770-726-27990
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Publication No. US20050266409A1
EMBERAL INFORMATION:
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM.01079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48840
SOFTWARE: Patentin version 3.2
SEQ ID NO 27536
LENGTH: 21
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APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.2%; Score 13; DB 6; Length 21;
84.6%; Pred. No. 2.38+03;
ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27537, Application US/10770726 Ublication No. US20050266409A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 27539, Application US/10770726
Publication No. US20050266409A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Brown, Bugene
                                                                                                                                                                                                                                                                  5 GAGUGAUGGCAAG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 GAGTGATGGCAAG 18
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Best Local Similarity 84.6
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-770-726-27536
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US-10-770-726-27539
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Publication No. US20050266409A1
GENERAL INPORMATION:
APPLICANT: Wyeln
APPLICANT: Brown, Bugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION NUMBER: 105/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SEQ ID NO 28076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  General Information of July 10770726

Publication No. US20050266409A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wyeth, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING, TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
LENGTH: 21
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Publication No. US20050266409A1

GENERAL INFORMATION:
APPLICANT WPET

APPLICANT LIU, Wei
APPLICANT: LIU, Wei
TITLE OF INVENTION: CANCERS
TITLE OF INVENTION: CANCERS
TITLE OF INVENTION: CANCERS
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
SEQ ID NO 28079
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Pred. No. 2.3e+03;
2; Mismatches 0
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Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                       TYPE: DNA
CORGANISM: Homo sapiens
US-10-770-726-28076
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; ORGANISM: RNAi
US-10-770-726-28077
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US-10-770-726-28079
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US-10-770-726-28077
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Publication No. US20050266409A1

GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION WHOMER: US/10/770,726
CURRENT PAILNG DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
SEQ ID NO 28074
LENGTH: 21
                                                                                                                                                                                                                                         Sequence 28073, Application US/10770726

Publication No. US20050266409A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wyeth

APPLICANT: Liu, Wei

APPLICANT: APPLICANTION: CANCERS

CURRENT APPLICATION UNDER: US/10/770,726

CURRENT APPLICATION UNDER: 2044-02-04

NUMBER OF SEQ ID NOS: 48640

SEQ ID NO 28073

LENGTH: 21
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Pred. No. 2.3e+03;
---hag 0; Indels
            Score 13; DB 6; Lengtn 41;
Pred. No. 2.38+03;
0; Indels
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Pred. No. 2.3e+C
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100.0%; Pred. No. -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 34
US-10-770-726-28076
; Sequence 28076, Application US/10770726
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                             54.2%;
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Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                             6 GAGTGATGGCAAG 18
                                                                                                                                1 GAGUGAUGGCAAG 13
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Best Local Similarity 100.
Matches 13; Conservative
                                              Best Local Similarity 84.6
Matches 11, Conservative
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US-10-770-726-28073
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US-10-770-726-28074
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US-10-770-726-28073
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US-10-770-726-28074
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                                 Query Match
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                                           53.3%; Score 12.8; DB 8; Length 19; 75.0%; Pred. No. 2.8e+03; tive 2; Mismatches 2; Indel8
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GENERAL INVENTATION:

APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Resynolds, Angela
APPLICANT: Resynolds, Angela
APPLICANT: Resynolds, Edeke, Devin
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 394642

LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Charmacon, Inc.
APPLICANT: Charmacon, Inc.
APPLICANT: Charmacon, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephn
APPLICANT: Scaringe, Stephn
APPLICANT: Marshall, William
APPLICATION NUMBER: US/11/101,244
CURRENT PILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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                                                                                                                                                                                                                                                                                                                    Sequence 394642, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
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                                                                                                                                                                             2 GGAGUGACUGCAAGCA 17
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SOFWARE: Proprietary
SEQ ID NO 394667
LENGTH: 19
                                      Ouery Match
Best Local Similarity 75.01
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Conservative
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; ORGANISM: Homo sapiens
US-11-101-244-394642
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US-11-101-244-394667
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Matches 13; Conserva
                                                                                                                                                                                                                                                                      RESULT 39
US-11-101-244-394642
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US-11-101-244-394667
  US-11-101-244-385942
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US-10-933-294A-17960

is Sequence 17960, Application US/10939294A

is Dublication No. US20050266417A1

is GENERAL INFORMATION:

APPLICANT: Barany, Francis

APPLICANT: Pingle, Maneah

APPLICANT: Pingle, Maneah

TITLE OF INVENTION: Machode for identifying target nucleic acid molecules

FILE REFERENCE: 19603/4121 (CRF D-2995-02)

CURRENT APPLICATION NUMBER: US/10/939,294A

CURRENT APPLICATION NUMBER: US 60/502/731

PRIOR FILING DATE: 2003-09-10

PRIOR FILING DATE: 2003-09-12

NUMBER OF SEQ ID NOS: 38895

SEQ ID NO 17960

LENGTH: 32
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US-11-101-244-385942
Sequence 385942, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
APPLICANT: Diarmacon, Inc.
; APPLICANT: Reynolds, Ansatasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
; TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT PILING DATE: 2005-04-07
; PRIOR FILING DATE: 2005-01-0
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; LEMCHARI: Proprietary
; LEMCHARI: Proprietary
                                                                                                                     Query Match 54.2%; Score 13; DB 6; Length 21; Best Local Similarity 100.0%; Pred. No. 2.3e+03; Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 54.2%; Score 13; DB 6; Length 32; Best Local Similarity 76.2%; Pred. No. 2.3e+03; Matches 16; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: oligonucleotide probe US-10-939-294A-17960
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                                                                                                                                                                                                                        6 GAGTGATGGCAAG 18
                                                                                                                                                                                                                                                    1 GAGTGATGGCAAG 13
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: RNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial
                                                                         US-10-770-726-28079
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Ouery Match

53.3%; Score 12.8; DB 8; Length 19;

Best Local Similarity 81.2%; Pred: No. 2.8e+03;

Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCA 20

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Db 1 GGAGTGATGGCAAGCA 16

Search completed: December 13, 2005, 16:24:34

Job time: 214.5 secs
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300.705 Million cell updates/sec
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                                                                                                                                                   December 13, 2005, 13:21:57; Search time 660 Seconds
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1: /cgn2_6/ptodata/1/pubpna/USO7 PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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9: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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                          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Match Length DB
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Sequence 8888, Ap Sequence 607979, Sequence 607979, Sequence 15256, A Sequence 15277, A Sequence 15277, A Sequence 4241, Ap Sequence 4241, Ap Sequence 4335, Ap Sequence 4335, Ap Sequence 3549, Ap Sequence 3549, Ap Sequence 1927, Ap Sequence 1910, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4293, Ap
Sequence 4302, Ap
Sequence 4309, Ap
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Sequence 4303, Application US/09780533A
Publication No. US20030060611A1
GRNERAL INFORMATION:
APPLICANT: Ribacyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Haeberli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
TITLE NE PRERENCE: MRH800, 878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Sequence 2, Application US/10713137

Bublication No. US20050106573A1

GENERAL INFORMATION:

APPLICANT: Pabla, Abdul Qadar Mohammad

APPLICANT: Alban, Aarif

TITLE OF INVENTION: A method of detection of predisposition

TITLE OF INVENTION: A method of detection of predisposition

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TITLE OF INVENTION: A 
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                                                                                            US-10-669-841-8888
US-10-182-049-35
US-10-719-956-607979
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Best Local Similarity 100.
Matches 24; Conservative
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Roswiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
ITILE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
FILE REFERENCE: MBHB00-882-C (400/019)
CURRENT APPLICATION NUMBER: US/09/653,225
PRIOR APPLICATION NUMBER: US/09/653,225
PRIOR PLING DATE: 2000-08-31
PRIOR PLING DATE: 2000-08-31
PRIOR PLING DATE: 2000-08-31
PRIOR PLING DATE: 1999-06-31
NUMBER OF SEQ ID NOS: 5586
SOFTWARE: Patentin version 3.0
SEQ ID NO 4389
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TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
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                                                                                                                   ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-1941
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80.0%; Pred. No. 4.3e+02;
tive 2; Mismatches 2;
                                                                                                                                                                                                                         Query Match 71.7%; Score 17.2; DB 3; Best Local Similarity 77.3%; Pred. No. 2.7e+02; Matches 17; Conservative 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 223011, Application US/11060756 Ubblication No. US20050221354A1 GENERAL INPORMATION:
APPLICANT: Wyeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 4389, Application US/10712672; Publication No. US20040102413A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         2 AGAGGAGUGAUGGCAUGCACUA 23
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                                                                   TYPE: RNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin version 3.2
SEQ ID NO 223011
LENGTH: 25
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ORGANISM: probe
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US-10-712-672-4389
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                  SEQ ID NO 1941
                                          LENGTH: 37
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Publication No. US20030087847A1

GENERAL INFORMATION:

APPLICANT: Booher:

APPLICANT: Booher:

APPLICANT: Booher:

APPLICANT: Booher:

APPLICANT: Rettaey, Ali

APPLICANT: Rettaey, Ali

TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK
TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK
TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK
TITLE OF INVENTION: MEXAME

FILE REPRENCE: MBHB00-955-A (400/008)

CURRENT APPLICATION NUMBER: US 60/179,983

PRIOR APPLICATION NUMBER: US 60/179,983

PRIOR FILING DATE: 2000-02-02

PRIOR FILING DATE: 2000-03-02

NUMBER OF SEQ ID NOS: 2992

SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-533A-4303
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Sequence 2709, Application US/09730289B

Sequence 2709, Application US/09730289B

Sequence 2709, Application US/09730289B

Sequence 2709, Application US/08080B

Hard Candra No. US20030050259A1

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Blatt, Larry

APPLICANT: Blatt, Larry

APPLICANT: McSwiggen, Jim

TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease

FILE REFERENCE: MBHB00-864-A (400/006)

CURRENT APPLICATION NUMBER: US 60/169,100

PRIOR FILING DATE: 2000-12-06

NUMBER OF SEQ ID NOS: 3897

SOFTWARE: PALENTING DATE: 1999-12-06

NUMBER OF SEQ ID NOS: 3897
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71.7%; Score 17.2; DB 3; Length 37;
Best Local Similarity 77.3%; Pred. No. 2.7e+02;
Matches 17; Conservative 2; Mismatches 3; Indels
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Best Local Similarity 78.3%; Pred. No. 90;
Matches 10; Conservative 2; Mismatches
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PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: Patentin version 3.0
SEQ ID NO 4303
LENGTH: 37
                                                                                                                                   TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
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US-09-776-474-1941
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LENGTH: 37
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TYPE: RNA
ORGANISM: Artificial Sequence
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US-09-780-533A-4266
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Sequence 2718, Application US/09730289B

Publication No. US20030050259A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.,

APPLICANT: Ribozyme Pharmaceuticals, Inc.,

APPLICANT: Blatt, Larry

APPLICANT: McSwiggen, Jim

TITLE OF INTURINION Method and Reagent for Treatment of Cardiac Disease

FILE RFERENCE: MBHB00-864-A (409/730,289B

CURRENT APPLICATION NUMBER: US 60/169,100

PRIOR APPLICATION NUMBER: US 60/169,100

PRIOR FILING DATE: 1999-12-06

NUMBER OF SEQ ID NOS: 3897

SOFTHARE: PAECHLIN Version 3.0
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APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Chowitz, Bharat
APPLICANT: Haeberlia, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MSHB00, 878-A (400/011)
FURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR PILING DATE: 2000-02-11
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                                        69.2%; Score 16.6; DB 10; Length 25; 82.6%; Pred. No. 5.3e+02; ive 0; Mismatches 4; Indels
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69.2%; Score 16.6; DB 3;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4;
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Pred. No. 5.3e+02;
2; Mismatches 4;
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SOFWARE: Patentin version 3.0
SEQ ID NO 4266
LENGTH: 37
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ORGANISM: Artificial Sequence
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Best Local Similarity 73.9
Matches 17; Conservative
                                                                  Best Local Similarity 82.6
Matches 19; Conservative
US-11-060-756-223011
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US-09-780-533A-4266
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LENGTH: 37
                                               Query Match
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APPLICANT: Ribozyne Pharmaceuticals, Inc
APPLICANT: Ribozyne Pharmaceuticals, Inc
APPLICANT: McSwiggen, Jim
APPLICANT: Tompson, Jim
APPLICANT: Arengeon, Jim
APPLICANT: Ayers, Dave
APPLICANT: Szymkowski, Edmund
APPLICANT: Szymkowski, Edmund
TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlox
TITLE OF INVENTION: Channel-1
FILE REPERENCE: 249/021
CURRENT APPLICATION NUMBER: US/09/927,046
CURRENT FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 5450
SEQ ID NO 3502
LENGTH: 37
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APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Mcxfagen, Jim
APPLICANT: Mcxfager, Jim
APPLICANT: Mcxfager, Jim
APPLICANT: Mcxfager, Jim
APPLICANT: Mcxfager, Jim
FILE REFERENCE: MBHB00-845-H (400/029)
CURRENT APPLICATION NUMBER: US/09/877,478
CURRENT APPLICATION NUMBER: US 09/632,712
PRIOR FILING DATE: 2000-10-2-14
PRIOR PLING DATE: 2000-03-20
PRIOR PLING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/696,347
PRIOR APPLICATION NUMBER: US 09/696,347
PRIOR PLING DATE: 2000-06-09
PRIOR PLING DATE: 1994-02-07
PRIOR PLING DATE: 1995-05-04
PRIOR APPLICATION NUMBER: US 08/434,504
PRIOR PLING DATE: 1995-05-04
PRIOR PLING DATE: 1995-05-04
PRIOR APPLICATION NUMBER: US 09/436,430
PRIOR PLING DATE: 1995-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-927-046-3502
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69.2%; Score 16.6; DB 3;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4;
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Publication No. US20030068301A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                        Sequence 3502, Application US/09927046 Publication No. US20030064946A1 GENERAL INFORMATION:
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RESULT 13
US-09-930-423-2765
Sequence 2765, Application US/09930423
; Sequence 2765, Application US/09930423
; Fublication No. US2003092003A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Larry
; APPLICANT: Blatt, Larry
; APPLICANT: Blatt, Larry
; APPLICANT: Blatt, Larry
; TILE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REPERENCE: MBH800, 318-A 400/027
; CURRENT APPLICATION NUMBER: 2001-08-15
; CURRENT PILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2765
; LENGTH: 37
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APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
FILE REFERENCE: MBHB00, 918-A 400/027
CURRENT APPLICATION NUMBER: US/09/930, 423
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 4553
SOFTWARE: Patentin version 3.0
SEQ ID NO 2786
LENGTH: 37
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69.2%; Score 16.6; DB 3;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4;
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  Mismatches
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; Publication No. US20030143708A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 2786, Application US/09930423; Publication No. US20030092003A1; GENERAL INFORMATION:
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  2;
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  17; Conservative
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US-09-745-237A-2746
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US-09-930-423-2786
     Matches
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Sequence 2764, Application US/09930423

Sequence 2764, Application US/09930423

Sequence 2764, Application No. US20030032003A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Blatt, Larry

APPLICANT: Blatt, Larry

APPLICANT: Blatt, Larry

TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease

FILE REFERENCE: MBHB00, 918-A 400/027

CURRENT PAPLICATION NUMBER: US/09/930,423

CURRENT PILING DATE: 2001-08-15

NUMBER OF SEQ ID NOS: 4553

SOFTWARE Patentin version 3.0

SEQ ID NO 2764

LENGTH: 37
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Sequence 2746, Application US/09930423
Publication No. US20030092003A1
GENERAL INFORMATION:
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Mathod and Reagent for the Treatment of Alzheimer's Disease
FILE REFERENCE: Method and Reagent for the Treatment of Alzheimer's Disease
FILE REFERENCE: MHB00,918-A 400/027
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 4553
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2746
LENGTH: 37
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; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-930-423-2746
                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
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Pred. No. 5.3e+02;
                                                                                                                                                                                                                           Query Match
69.2%; Score 16.6; DB 3; Length 37;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4; Indels
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SOFTWARE: PatentIn version 3.0 SEQ ID NO 4013 LENGTH: 37
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                                                                                                   ORGANISM: Artificial Sequence
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Best Local Similarity
                                                                                                                                                                            US-09-877-478-4013
                                                                              TYPE: RNA
                                                                                                                          FEATURE:
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Query Match
Best Local Similarity
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US-09-745-237A-2786
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LENGTH: 37
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APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Mcthod and Reagent for the Treatment of Alzheimer's Disease
FILE REFERENCE: 400/007 (MBHB00-918-A)
CURRENT APPLICATION NUMBER: US/09/745,237A
CURRENT FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 4550
SEQ ID NO 2764
LENGTH: 37
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US-09-745-237A-2764
                                   APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Wethod and Reagent for the Treatment of Alzheimer's Disease
FILE REFERENCE: 400/007 (MBHB00-918-A)
FILE REFERENCE: 400/007 (MBHB00-918-A)
CURRENT APPLICATION VUMBER: US/09/745,237A
CURRENT FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 4550
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2746
LENGTH: 37
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CTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-09-745-237A-2746
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69.2%; Score 16.6; DB 3;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4;
                     APPLICANT: Ribozyme Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2764, Application US/09745237A Publication No. US20030143708A1 GENERAL INFORMATION:
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GENERAL INCOMMATION:

APPLICANT: Sirna Therapeutice, Inc.
APPLICANT: Sirna Therapeutice, Inc.
APPLICANT: Draper, Kenneth
APPLICANT: Draper, Kenneth
APPLICANT: Malat, Larry
APPLICANT: McSwiggen, Jim
APPLICATION NUMBER: US/10/142,902
CURRENT FILING DATE: 2003-01-15
PRIOR PLING DATE: 2000-03-20
PRIOR PLING DATE: 2000-03-20
PRIOR PLING DATE: 2000-03-20
PRIOR PLING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/636,347
PRIOR PLING DATE: 2000-01-24
PRIOR FILING DATE: US 08/193,627
PRIOR PLING DATE: US 08/193,627
PRIOR FILING DATE: US 08/193,627
PRIOR FILING DATE: US 08/193,627
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US-09-745-237A-2786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
FILE REFERENCE: 400/007 (MBHB00-918-A)
FILE REPERENCE: 400/007 (MBHB00-918-A)
CURRENT APPLICATION NUMBER: US/09/745,237A
CURRENT FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 4550
SEQ ID NO 2786
LENGTH: 37
LENGTH: 37
                                            ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid US-09-745-237A-2765
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Pred. No. 5.3e+02;
2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 2786, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; sequence 4013, Application US/10342902; Publication No. US20040054156A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
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Best Local Similarity 73.9
Matches 17, Conservative
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y applicant; bloozyme Pharmaceuticals, Inc., APPLICANT; Blatt, Larry
APPLICANT; Mcswiggen, Jim
APPLICATION WUMBER; US/09/877,478
CURRENT FILING DATE; 2000-03-20
PRIOR FILING DATE; 2000-03-20
PRIOR FILING DATE; 2000-03-09
PRIOR FILING DATE; 2000-00-09
PRIOR FILING DATE; 2000-10-07
PRIOR FILING DATE; 2000-10-07
PRIOR PELING DATE; 1994-02-07
PRIOR FILING DATE; 1995-05-04
PRIOR FILING DATE; 1999-110 NUMBER; US 09/436,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid US-09-780-533A-4274
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APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: McGwiggen, Jim
APPLICANT: Chowrira, Bharat
APPLICANT: Chowrira, Bharat
APPLICANT: Haeberli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
TITLE OF INVENTION: Method and 80/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
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Pred. No. 8.3e+02;
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76.2%; Pred. No. o...
2; Mismatches
      2; Mismatches
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publication No. US20030060611A1
GENERAL INFORMATION:
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Matches 16; Conservative
      17; Conservative
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US-09-780-533A-4274
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LENGTH: 37
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APPLICANT: Pamela, Pavco
APPLICANT: Bartice, Lee
APPLICANT: Kenneth, Draper
APPLICANT: Elisabeth, Roberts
TITLE OF INVENTION: OLIGONOCIECOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA
TITLE OF INVENTION: UTGNOTICEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA
TITLE OF INVENTION: UTGNOTICEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA
TITLE OF INVENTION: UTGNOTICEOTIDE
TITLE REFERENCE: 400/042US (MBHB02-249-E)
CURRENT APPLICATION NUMBER: US 60/296,876
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-09
PRIOR PILING DATE: 2001-10-24
PRIOR PAPLICATION NUMBER: US 60/335,059
PRIOR PILING DATE: 2002-03-01
PRIOR PILING DATE: 2002-03-01
PRIOR PILING DATE: 2002-03-01
PRIOR PILING DATE: 2002-03-01
PRIOR PILING DATE: 2000-02-13
PRIOR PILING DATE: 2000-02-13
PRIOR PILING DATE: 2000-01-19
PRIOR PILING DATE: 2000-02-15
                                                                                                                                                                                                                                               ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-342-902-4013
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US-10-669-841-8904
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Pred. No. 5.3e+02;
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Publication No. US20040127446A1
GENERAL INFORMATION:
APPLICANT: Lawrence, Blatt
APPLICANT: Dennis, Macejak
APPLICANT: Dennis, Macejak
APPLICANT: David, Morriseey
PRIOR APPLICATION NUMBER: US 09/436,430 PRIOR FILING DATE: 1999-11-08 NUMBER OF SEQ ID NOS: 6592 SCPTWARE: Patentin version 3.2 SEQ ID NO 4013 LENGTH: 37
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 8904
LENGTH: 37
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                                                                                                                                                                                      TYPE: RNA ORGANISM: Artificial Sequence
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Best Local Similarity
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ORGANISM: Artificial Sequence
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McSwiggen
                                                                                                      Patrice, Lee
Kenneth, Draper
                                                                 Pamela, Pavco
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| Sequence 3997, Application US/10342902
| Sequence 3997, Application US/10342902
| Publication No. US20040054156A1
| GENERAL INFORMATION:
| APPLICANT: Sirna Therapeutics, Inc. |
| APPLICANT: Darger, Kenneth |
| APPLICANT: Darger, Larry |
| APPLICANT: Morsissey, Dave |
| TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication |
| FILE REFERENCE: 400/075 (MEHBOO-845-1) |
| CURRENT PILING DATE: 2001-06-08 |
| PRIOR PILING DATE: 2001-06-08 |
| PRIOR PLICATION NUMBER: US 09/531,025 |
| PRIOR PLICATION NUMBER: US 09/531,025 |
| PRIOR PLICATION NUMBER: US 09/636,347 |
| PRIOR PLICATION NUMBER: US 09/636,347 |
| PRIOR PLICATION NUMBER: US 09/696,347 |
| PRIOR PLICATION NUMBER: US 09/696,347 |
| PRIOR PLICATION NUMBER: US 09/696,347 |
| PRIOR PLICATION NUMBER: US 09/436,430 |
| PRIOR PLICATION 
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                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-877-478-3997
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                                                                                                                                                                                                                                                                                                              67.5%; Score 16.2; DB 3; Length 37; 76.2%; Pred. No. 8.3e+02; Live 2; Mismatches 3; Indels
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US-10-669-841-8888
S. Sequence 8888, Application US/10669841
Publication No. US20040127446A1
GENERAL INFORMATION:
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APPLICANT: Lawrence, Blatt
APPLICANT: Dennis, Macejak
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ORGANISM: Artificial Sequence
       SOFTWARE: PatentIn version 3.0 SEQ ID NO 3997
LENGTH: 37
                                                                                                                                                     ORGANISM: Artificial Sequence
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Best Local Similarity 76.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 76.2<sup>3</sup>
Matches 16; Conservative
                                                                                                                    TYPE: RNA
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TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR APPLICATION NUMBER: US 60/536,639
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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                                                                                                                                                                                                                                                         Sequence 607979, Application US/10719956
| Publication No. US20040146910A1
| GENERAL INFORMATION:
| APPLICANT: We Mei Zhou
| TITLE OF INVENTION: Methods of Genetic Analysis of Rat
| FILE REFERENCE: 3527.1
| CURRENT APPLICATION NUMBER: US/10/719,956
| CURRENT FILING DATE: 2003-11-20
| PRIOR APPLICATION NUMBER: 60/427,836
| PRIOR FILING DATE: 2002.1.20
| NUMBER OF SEQ ID NOS: 699466
| SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
| LENGTH: 25
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                                    Query Match 66.7%; Score 16; DB 9; Length 18; Best Local Similarity 100.0%; Pred. No. 1e+03; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16; DB 7; Length 25;
Pred, No. 1e+03;
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US-11-036-317-435997
; Sequence 435997, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
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US-10-138-674-15256
; Sequence 15256, Application US/10138674
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|| || || || || || || || 11
1 GACTGATGGCAAGCATGAC 19
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Best Local Similarity 79.2%;
Matches 19; Conservative 0
                                                                                                                       9 TGATGGCAAGCACGAC 24
                                                                                                                                             ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-607979
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US-11-036-317-435997
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US-10-719-956-607979/c
US-10-182-049-35
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GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Bayco, Pam
APPLICANT: Bayco, Pam
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Oatme
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions RITLE OF INVENTION: Method and Reagent Enderthelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: 2002-05-03
UNBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0
SEQ ID NO 15266
LENGTH: 36
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Publication No. US20040077565A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Pavco, Pam

APPLICANT: Brinchcomb, Dan

APPLICAN
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Publication No. US20040102389A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.;
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 GGAGTGATGGCAAGCACGA 23
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ORGANISM: Artificial Sequence
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US20040077565A1
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US-10-712-672-4246

US-10-712-672-4246

Sequence 4246, Application US/10712672

Publication No. US20040102413A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Chowrira, Bharat
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jan
APPLICANT: McHood and Reagent for the Inhibition of Telomerase Enzyme
ITITE OF INVENTION: Whethod and Reagent for the Inhibition of Telomerase Enzyme
ITITE REFERENCE: MBH800-882-C (400/019)
CURRENT APPLICATION NUMBER: US/99/653,225
CURRENT APPLICATION NUMBER: 60/197,769
FRIOR FILING DATE: 2000-04-14
FRIOR FILING DATE: 1999-08-31
                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-712-672-4241
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APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
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illarity 78.9%; Pred. No. 1.3e+03;
Conservative 2; Mismatches 2;
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Publication No. US20040102413A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
PRIOR APPLICATION NUMBER: 2000-08-31
PRIOR PILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/197,769
PRIOR PILING DATE: 2000-04-14
PRIOR PILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 5586
SOFTWARE: Patentin version 3.0
SEQ ID NO 4241
LENGTH: 36
           APPLICATION NUMBER: US/09/653,225
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Best Local Similarity
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Matches 15; Conserva
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US-10-712-672-4375
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                                        APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
FILE REPERENCE: MHHBOG-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
CURRENT FILING DATE: 2003-04-11
NUMBER OF SEQ ID NGS: 20822
SOFTWARE: PatentIn version 3.0
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US-10-287-949A-15277
                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid US-10-287-949A-15256
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; Sequence 15277, Application US/102899AI
; Publication No. US20040102389AI
; GENERAL INFORMATION:
GAPLICANT: Ravco, Pam
; APPLICANT: Mayorigen, Jim
; APPLICANT: Mayorigen, Jam
; APPLICANT: Mayorigen, Mathod and Reagent for the Treatment of Diseases or Conditi
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH800-876-N (400/049)
; CURRENT PILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFFWARE PATENTIN VERSION 3.0
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APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
FILE REFERENCE: MBHB00-882-C (400/019)
CURRENT APPLICATION NUMBER: US/10/712,672
CURRENT FILING DATE: 2003-11-13
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Pred. No. 1.3e+03;
2; Mismatches 2;
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Pred. No. 1.3e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4241, Application US/10712672 Publication No. US20040102413A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 78.9
Matches 15, Conservative
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Matches 15; Conservative
                       Stinchcomb,
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US-10-287-949A-15277
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LENGTH: 36
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LENGTH: 36
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US-U9-927-046-3492
; Sequence 3492, Application US/09927046
; Publication No. US2003064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: Grupe, Andrew
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlori
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlori
; TITLE OF INVENTION: WHORER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3492
LIENGTH: 37
                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-533A-4335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid US-09-927-046-3492
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                     APPLICANT: Chowrira, Bharat
APPLICANT: Chowrira, Bharat
APPLICANT: Haeberli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MBHBOO, 878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT APPLICATION NUMBER: US 60/181,797
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: Patentin version 3.0
SEQ ID NO 4335
LENGTH: 37
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Best Local Similarity 78.9%; Pred. No. 1.3e+03;
Matches 15; Conservative 2; Mismatches 2;
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Pred. No. 1.3e+03;
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Best Local Similarity 78.9%; Pred. No. 1.3e
Matches 15; Conservative 2; Mismatches
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Sequence 3526, Application US/09927046

Publication No. US20030064946A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: MCSwiggen, Jim

APPLICANT: McKenzie, Tim
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                                                                                                                                                                                                                                                                                                                                        TYPE: RNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Publication No. US20040102413A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: ACSAigsen, Jim
APPLICANT: Acsaigsen, Jim
APPLICANT: Acsaigsen, Jim
APPLICANT: Binchcomb, Dan
TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
TITLE OF INVENTION: WORBER: US/09/613, 225
CURRENT FILING DATE: 2003-11-13
PRIOR PELICATION NUMBER: 60/197, 769
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 5586
SOUTH APPLICATION NUMBER: 60/197, 769
SEQ ID NO 4498
LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-712-672-4375
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US-10-712-672-4498
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               CURRENT APPLICATION NUMBER: US/10/712,672
CURRENT FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: US/09/653,225
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 2000-08-14
PRIOR FILING DATE: 2000-08-14
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 5586
SOFTWARE: PATCH NOS: 5586
LENGTH: 36
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FILE REFERENCE: MBHB00-882-C (400/019)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGAGUGAUGCAUGCACUA 20
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
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US-10-712-672-4498
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TITE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CI TITLE OF INVENTION: Braywe FILE REFERENCE: MBHB00-955-A (400/008)
CURRENT APPLICATION NUMBER: US/09/776,474
CURRENT PILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 60/179,983
PRIOR PILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 2992
SEQ ID NO 1927
LENGTH: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid US-09-776-474-1927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 65.8%; Score 15.8; DB 3; Length 37; Best Local Similarity 78.9%; Pred. No. 1.3e+03; Matches 15; Conservative 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: RNA
ORGANISM: Artificial Sequence
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; Sequence 3549, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McKenzie, Jim
; APPLICANT: Ayers, Dave
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Grupe, Andrew
; APPLICANT: Grupe, Andrew
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlori
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlori
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlori
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlori
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlori
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn Version 3.0
APPLICANT: Ayers, Dave
APPLICANT: Grupe, Andrew
APPLICANT: Szyncowski, Edmund
TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlori
TITLE OF INVENTION: Channel-1
FILE REPERBURG: 249/021
CURRENT APPLICATION NUMBER: US/09/927,046
CURRENT APPLICATION NUMBER: US/09/927,046
CURRENT FILING DATE: 2001-08-09
SOFTWARE: Patentin version 3.0
SEQ ID NO 3526
LENGTH: 37
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CTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-927-046-3549
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid US-09-927-046-3526
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APPLICANT: Jarvis, Thale
APPLICANT: Booher, Robert
APPLICANT: Holman, Patricia
APPLICANT: Fattaey, Ali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1927, Application US/09776474; Publication No. US20030087847A1; GENERAL INFORMATION:
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LENGTH: 37
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RESULT 2
US-09-371-772B-13000
; Sequence 13000, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
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1014, Ap
1014, Ap
4012, App
4013, Ap
4015, Ap
4016, Ap
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4019, Ap
12719, A
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12711, A
12725, A
14177, A
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Sequence 13000, A
                                                                                                                                                                             December 13, 2005, 13:14:34 ; Search time 104.5 Seconds (without alignments) 408.244 Million cell updates/sec
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1. /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2. /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3. /cgn2_6/ptodata/1/ina/6_COMB.seq:*
4. /cgn2_6/ptodata/1/ina/6_COMB.seq:*
5. /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6. /cgn2_6/ptodata/1/ina/PcTVS_COMB.seq:*
7. /cgn2_6/ptodata/1/ina/PcTVS_COMB.seq:*
8. /cgn2_6/ptodata/1/ina/PcTOMB.seq:*
9. /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9. /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-371-772B-12979
US-09-371-772B-13000
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US-09-371-772B-12711
US-09-371-772B-12711
US-09-371-772B-14177
US-09-371-772B-14177
US-09-479-005A-021
US-09-466-108A-4013
US-09-866-108A-4014
US-09-866-108A-4014
US-09-866-108A-4014
US-09-866-108A-4019
US-09-311-772B-12719
US-09-371-772B-12719
US-09-371-772B-1279
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Maximum Match 100%
Listing first 45 summaries
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Match Length
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Maximum DB seq length: 50
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Pavcó, Pam McSwiggen, Jim Stinchcomb, Dan

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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Roswigen, Jim
APPLICANT: Braco, Pam
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions I
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
CURRENT APPLICATION NUMBER: US/09/371,7728
CURRENT FILING DATE: 1999-08-10
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1996-10-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12979
LENGTH: 36
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US-09-371-772B-12979
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         14162, A
665, App
785, App
938, App
42756, A
                                                                                                                                                                                                                                               Sequence 12754, Sequence 12767, Sequence 12819, Sequence 12890, Sequence 12939, Sequence 12978, Sequence 13062, Sequence 13062
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Patent No. 5
Sequence 12
                                        Sequence
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US-09-371-772B-14162
US-09-479-005A-665
US-09-479-005A-785
US-09-3796-196G-42756
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US-09-371-772B-12724
US-09-371-772B-12724
US-09-371-772B-12764
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US-09-371-772B-12978
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US-09-371-772B-13978
US-09-371-772B-13978
US-09-371-772B-13978
US-09-371-772B-13978
US-09-371-772B-13065
US-09-371-772B-13065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 12979, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-371-772B-12979
         FEATURE
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TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor FILE REFERENCE: MBHB00, 876-J (237/198)

CURRENT APPLICATION NUMBER: US/09/371,772B

CURRENT FILING DATE: 1999-08-10

PRIOR APPLICATION NUMBER: US 60/005,974

PRIOR APPLICATION NUMBER: US 68/584,040

PRIOR FILING DATE: 1996-01-08

NUMBER OF SEQ ID NOS: 14225

SOFTHARE: PatentIn version 3.0

SEQ ID NO 12711

LENGTH: 36
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PRIOR PILING DATE: 1995-10-26
PRIOR PILING DATE: 1995-10-26
PRIOR PILING DATE: 1995-10-08
RIOR PAPLICATION NUMBER: US 08/584,040
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
SEQ ID NO 12725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid US-09-371-772B-12711
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US-09-371-772B-12725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.3%; Score 15.2; DB 3; 75.0%; Pred. No. 8.3e+02; tive 2; Mismatches 3;
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Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
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; APPLICANT: Ribozyme Pharmaceuticals, Inc.
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US-09-371-772B-14177
; Sequence 14177, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
ORGANISM: Artificial Sequence
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Best Local Similarity 75.04
Matches 15; Conservative
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Best Local Similarity 75.0°
Matches 15; Conservative
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US-09-371-772B-12725
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                 TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor FILE REFERENCE: MBHB00, 275-47 (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-10-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid US-09-371-772B-13000
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US-09-479-005A-597
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| Sequence 597, Application US/09479005A |
| Patent No. 6656731 |
| GENERAL INFORMATION: |
| APPLICANT: Ribozyme Pharmaccuticals, Inc. |
| TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity |
| FILE REFERENCE: MBHB00-884-C |
| CURRENT APPLICATION NUMBER: US 09/444,209 |
| PRIOR APPLICATION NUMBER: US 09/444,209 |
| PRIOR FILING DATE: 1998-11-19 |
| PRIOR FILING DATE: 1998-09-22 |
| PRIOR FILING DATE: 1998-09-22 |
| NUMBER OF SEQ ID NOS: 1208 |
| SOFTWARE: Patentin version 3.0 |
| SEQ ID NO 597 |
| LENGTH: 36
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PAPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
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; Sequence 12711, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 13000
LENGTH: 36
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Escobedo, Jaime
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Gaps

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; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid US-09-479-005A-825
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US-09-479-005A-1014
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FALEL NO. 9020/31

FALEL NO. 9020/31

FILE REFERENCE: MBHB00-884-C

CURRENT APPLICATION NUMBER: US/09/479,005A

CURRENT FILING DATE: 2000-01-07

FRIOR PELICATION NUMBER: US 09/444,209

PRIOR APPLICATION NUMBER: US 09/159,274

PRIOR PILING DATE: 1998-09-22

PRIOR FILING DATE: 1998-09-22

FRIOR FILING DATE: 1997-09-22

NUMBER OF SEQ ID NOS: 1208

SOFTWARE: Patentin version 3.0
                 APPLICANT: Ribozyme Pharmaceuticals, Inc.
TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
FILE REPERENCE: MBHB00-884-C
CURRENT FILING DATE: 1050-61-07
PRIOR PILING DATE: 2000-01-07
PRIOR PLING DATE: 1999-11-19
PRIOR PLING DATE: 1999-11-19
PRIOR PLING DATE: 1999-09-22
PRIOR PLING DATE: 1997-09-22
PRIOR PLING DATE: 1997-09-22
PRIOR PLING DATE: 1997-09-22
NUMBER OF SEQ ID NOS: 1208
SOFTWARE: Patentin Version 3.0
SOFTWARE: Patentin Version 3.0
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; Sequence 27, Application US/09430221
; Patent No. 6521425
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                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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APPLICANT: Perler, Francine
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Matches 15; Conservative
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nes 15, Conserva
  GENERAL INFORMATION:
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Matches
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Sequence 14200, Application US/09371772B

Patent No. 6566127

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: Bacobedo, Jaime
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Broobedo, Jaime
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels 0.69/0971, 772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR PILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 14200
LENGTH: 36
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Estinchcomb, Dan
APPLICANT: Estinchcomb, Dan
APPLICANT: Estinchcomb, Dan
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Menboo, 876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1995-08-10
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PATENT OF APPLICATION NUMBER: US 68/584,040
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US-09-371-772B-14177
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Pred. No. 8.3e+02;
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US-09-479-005A-825
; Sequence 825, Application US/09479005A
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                                                                                                                                                                                                                                                                                                                                                                                   TYPE: RNA
ORGANISM: Artificial Sequence
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Best Local Similarity 75.0°
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                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 14177
LENGTH: 36
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APPLICANT: KANN, DATAL K.

APPLICANT: GIEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILER REFERENCE: AEONICA-7
CURRENT APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-09-27
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
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NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 686188
SEQ ID NO 4013
LENGTH: 25
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Pred. No. 1.2e+03;
   Mismatches
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GENERAL INFORMATION: APPLICANT: GU, Yizhong APPLICANT: GT, Yonggang APPLICANT: PENN, Sharron G, APPLICANT: HANZEL, David K.
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10.09-866-108A-4013
10.59 Sequence 40113, Application US/09866108A
10.6686188
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                                                             5 GGAGTGATGGCAAGCACG 22
                                                                                                                             GGAGTGAAGGGAAGCACG 25
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88.9%;
                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: GI, Yongang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David K.
APPLICANT: CHEN, Wensheng
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   Conservative
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Best Local Similarity 88.5
Matches 16; Conservative
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   16;
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APPLICANT:
APPLICANT:
   Matches
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APPLICANT: No. 666188

APPLICANT: GU, Yizhong
APPLICANT: GI, Yonggan
APPLICANT: RANK, David K.
APPLICANT: RANK, David K.
APPLICANT: SIANNON, MARK
TITLE OF INVENTION WYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERENCE: AEGOING.
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATI
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                    TITLE OF INVENTION: Screening And Use Of Reagents Which Block Or Activate TITLE OF INVENTION: Intein Splicing Utilizing Natural Or Homologous Exteins FILE OF INVENTION: Intein Splicing (FRAN/ERIC)
CURRENT APPLICATION NUMBER: US/09/430,221
EARLIER APPLICATION NUMBER: 08/911,492
EARLIER APPLICATION NUMBER: 08/811,492
EARLIER FILING DATE: 1997-03-05
NUMBER OF SEQ ID NOS: 46
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. 1e+03;
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US-09-866-108A-4012
Sequence 4012, Application US/09866108A
; Patent No. 6686188
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88.9%;
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SEQ ID NO 27
LENGTH: 39
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US-09-866-108A-4012
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Best Local Similarity
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FILING DATE: 2001-01-30
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Best Local Similarity 88.9
Matches 16; Conservative
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
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APPLICANT: RANK, David R.
APPLICANT: CHEN, Wenbheng
APPLICANT: SHANNON, MARK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT PILING DATE: 2001-05-25
PRIOR PILING DATE: 2000-05-26
RICH RAPPLICATION NUMBER: GS 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GS 60/206,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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                        TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
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NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 4014
LENGTH: 25
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Pred. No. 1.2e+03;
0; Mismatches 2;
                                                                                  FILE REFERENCE: AEOMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108A

CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-10-04

PRIOR PILING DATE: 2000-10-04

PRIOR PILING DATE: 2000-10-07

PRIOR PILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
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APPLICANT: GU, Yizhong
APPLICANT: TI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 88.9
Matches 16; Conservative
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US-09-866-108A-4015
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APPLICANT: AAVELL, DAVIG K.
APPLICANT: AAVELL, DAVIG K.
APPLICANT: AAVELL, DAVIG K.
APPLICANT: CHEN, Wensheng
APPLICANT: SANK, DAVIG R.
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,656
PRIOR PRILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Abomica Sequence Listing Engine
Patent No. 6666188
SEQ ID NO 4016
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Pred. No. 1.2e+03;
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88.9%;
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APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: H, Yonggang
APPLICANT: H, Yonggang
APPLICANT: H, Yonggang
APPLICANT: HANK, David K.
APPLICANT: HANK, David K.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
ITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: ABOMICA-7
CURRENT SHILNON MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE OF INVENTION MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE OF INVENTION MYOSIN-LIKE GENE EXPRESSED
FRIOR APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2000-05-26
FRIOR APPLICATION NUMBER: US 60/236,359
FRIOR FILING DATE: 2000-09-27
FRIOR APPLICATION NUMBER: PCT/US01/00666
FRIOR FILING DATE: 2001-01-30
FRIOR FILING DATE: 2001-01-30
FRIOR FILING DATE: 2001-01-30
FRIOR FILING DATE: 2001-01-30
                                   APPLICANT: SHANNON, MARK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT PLE KEKENCE: 2001-05-25
FRIOR APPLICATION NUMBER: US 60/207,456
FRIOR PELICATION NUMBER: US 60/207,456
FRIOR PELICATION NUMBER: US 60/236,359
FRIOR FILING DATE: 2000-09-27
FRIOR FILING DATE: 2000-09-27
FRIOR FILING DATE: 2001-01-04
FRIOR FILING DATE: 2001-01-03
FRIOR FILING DATE: 2001-01-03
FRIOR FILING DATE: 2001-01-30
FRIOR APPLICATION NUMBER: PCT/USO1/00663
FRIOR FILING DATE: 2001-01-30
FRIOR 
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Pred. No. 1.2e+03;
0; Mismatches 2;
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Patent No. 6686188
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88.9%;
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Best Local Similarity 88.9
Matches 16; Conservative
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: HANZEL, David K.

APPLICANT: HANZEL, David R.

APPLICANT: RANK, David R.

APPLICANT: RANK, David R.

APPLICANT: RANK, David R.

APPLICANT: SHANNON, Wark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE PILE REFERENCE: AEOMICA-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-09-25

PRIOR FILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-10-04

PRIOR PILING DATE: 2000-10-04

PRIOR PILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: GB 60/236,359

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30
                                           Gaps
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61.7%; Score 14.8; DB 3; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels
                                           Indels
   Pred. No. 1.2e+03;
0; Mismatches 2;
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Patent No. 6686188
SEQ ID NO 4017
LENGTH: 25
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Patent No. 6666188
GENERAL INFORMATION:
APPLICANT: GI, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: BIN, Sharron G.
APPLICANT: RANK, David K.
APPLICANT: RANK, David R.
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4017, Application US/09866108A Patent No. 6686188
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88.98;
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                                       16; Conservative
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US-09-866-108A-4017
Best Local Similarity
Matches 16; Conserva
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US-09-866-108A-4017
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Gaps

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APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-10-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
SEQ ID NO 17777
LENGTH: 36
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; Sequence 12964, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Rewiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Escobedo, Jaime
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditi;
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditi;
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditi;
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditi;
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditi;
TITLE OF INVENTION WHERE: US 60/005,974
; FILE REFERENCE: MBHB00,876-3 (237/198)
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR PLING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12264
LENGTH: 36
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, OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
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Pred. No. 1.3e+03;
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; Sequence 13173, Application US/09371772B
; Patent No. 6566127
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 77.8%;
Matches 14; Conservative
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APPLICANT: Stinchcomb, Dan
APPLICANT: Bacobedo, Jaime
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE REPERENCE: MBHB00, 387-7 (237/198)
CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR TILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
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PRIOR APPLICATION NUMBER: PCT/USO1/00669

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 15755

SOFTWARE: Acomica Sequence Listing Engine

Patent No. 6686188

LENGTH: 25

LENGTH: 25
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Pred. No. 1.2e+03;
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Pred. No. 1.3e+03;
2; Mismatches 2;
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APPLICANT: Pavco, Pam APPLICANT: Pavco, Pam APPLICANT: McSwiggen, Jim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-371-772B-12719
; Sequence 12719, Application US/09371772B
; Patent No. 6566127
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Best Local Similarity 88.9%;
Matches 16; Conservative C
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Best Local Similarity 77.8%;
Matches 14; Conservative
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 20
US-09-371-772B-12797
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LENGTH: 36
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Sequence 14110, Application US/09371772B

Patent No. 6566127

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Bavco, Pam
APPLICANT: Pavco, Pam
APPLICANT: Stinchcomb, Jam
APPLICANT: Stinchcomb, Jam
APPLICANT: Stinchcomb, Jam
APPLICANT: Brobedo, Jaime
APPLICANT: Brobedo, Jaime
APPLICANT: Brobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re;
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 14110
LENGTH: 36
LENGTH: 36
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US-09-371-772B-14110
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Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 14; Conservative 2; Mismatches 2; Indels
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Best Local Similarity 77.8<sup>3</sup>
Matches 14; Conservative
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Rabozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Bacobed, Jaim
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stochedo, Jaim
APPLICANT: Stochedo, Jaim
APPLICANT: Stochedo, Jaim
APPLICANT: Bacobedo, Jaim
FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-00-10
PRIOR FILING DATE: 1995-01-08
PRIOR FILING DATE: 1995-01-08
NUMBER OF SEQ ID NOS: 14225
SSCTARRE: PatentIn version 3.0
LENGTH: 36
                                                          APPLICANT: StinchComb, Jam
APPLICANT: StinchComb, Dan
APPLICANT: Stobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00, 876-J (237/198)
FRIOR PILING DATE: 1999-08-J0
PRIOR PELING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SEQ ID NO 13173
LENGTH: 36
LENGTH: 36
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US-09-371-772B-14087
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61.7%; Score 14.8; DB 3; Length 36;
Best Local Similarity 77.8%; Pred. No. 1.38+03;
Matches 14; Conservative 2; Mismatches 2; Indels
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Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 14; Conservative 2; Mismatches 2;
                     APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
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ORGANISM: Artificial Sequence
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US-09-371-772B-14087
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                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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RESULT 24 US-09-371-772B-14110

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US-09-396-196G-42756/C

US-09-396-196G-42756/Application US/09396196G

; Sequence 42756, Application US/09396196G
; Patent No. 6821724
; GENERAL INPORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: David Mack
; TITLE OF INVENTION: Methods of Genetic Analysis
; TITLE OF INVENTION: Methods of Genetic Analysis
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 14.8; DB 3;
Pred. No. 1.3e+03;
2; Mismatches 2;
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Application US/09479005A
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: RNA
ORGANISM: Artificial Sequence
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Best Local Similarity 77.8%;
Matches 14; Conservative
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Best Local Similarity 75.0°
Matches 18; Conservative
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US-09-479-005A-665
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; Sequence 785, Application US/09479005A
; Patent No. 6656731
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTYON: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFREENCE: MBHB00-884-C
; CURRENT APPLICATION NUMBER: US 09/479,005A
; CURRENT FILING DATE: 1999-11-19
; PRIOR FILING DATE: 1998-09-22
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: US 60/059,473
; PRIOR APPLICATION NUMBER: US 60/059,473
; PRIOR FILING DATE: 1998-09-22
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: PATENT VERSION 3.0
                                                          Sequence 665, Application US/09479005A
; Sequence 665, Application US/09479005A
; Patent No. 6656731
; GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
FILE REFRENCE: MBHB00-884-C
; CURRENT APPLICATION NUMBER: US/09/479,005A
; CURRENT FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 09/159,274
; PRIOR FILING DATE: 1999-11-19
; PRIOR FILING DATE: 1999-09-22
; RIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: PATENT NOS: 1208
; SOFTWARE: PATENT NOS: 1208
; SEQ ID NO 665
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US-09-479-005A-938
                                   SULT 26
-09-479-005A-665
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LENGTH: 36
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; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid US-09-479-005A-938
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT'S RIDOSYME PHARMACCULICALS, INC.
TILE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
FILE REFERENCE: MBHB00-884-C
CURRENT APPLICATION NUMBER: US/09/479,005A
CURRENT APPLICATION NUMBER: US 09/444,209
PRIOR APPLICATION NUMBER: US 09/159,274
PRIOR FILING DATE: 1998-01-19
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1997-09-22
PRIOR FILING DATE: 1998-09-22
PRIOR POSEQ ID NOS: 1208
SOFTWARE PATENTIN VERSION 3.0
SEQ ID NO 938
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;Patent No. 5519127
APPLICATT: SHAH, JYOTSNA;BUHARIN, AMELIA;LANE, DAVID J.
TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE DETECTION OF
;PNEUMOCYSTIS CANDINI
;NUMBER OF SEQUENCES: 57
;CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 36;
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APPLICANT: McGwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Bescobedo, Jaine
APPLICANT: Bescobedo, Jaine
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MHSBO, 876-37(198)
CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1996-10-08
NUMBER OF SEQ ID NOS: 14225
SOGTWARE: PatentIn version 3.0
SEQ ID NO 12754
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Sequence 12767, Application US/09371772B

SERVERAL INFORMATION:
APPLICANT: Riboxyme Pharmaceuticals, Inc.
APPLICANT: Roxiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Scobedo, Jane
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid US-09-371-772B-12727
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                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                             Length
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US-09-371-772B-12754
                                                                                                                                                                                                                                                                                                        Score 14.2; DB 3;
Pred. No. 2.4e+03;
                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 33
US-00-371-772B-12754
US-00-371-772B-12754, Application US/09371772B
Sequence 12754, Application US/09371772B
SERREAL INFORMATION:
APPLICANT: Pavco, Pam
APPLICANT: Pavco, Pam
PRIOR APPLICATION NUMBER: US 08/584,040 PRIOR FILING DATE: 1996-01-08 NUMBER OF SEQ ID NOS: 14225 SOFTWARE: Patentin version 3.0 SEQ ID NO 12727 LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GAAGUGAUGGCAUGCACUA 20
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Best Local Similarity 73.7%;
Matches 14; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity 73.7<sup>3</sup>
Matches 14, Conservative
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                                                                                                                                                            TYPE: RNA
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APPLICANT: McSwiggen, Jim
APPLICANT: Estobedo, Jaime
APPLICANT: Estobedo, Jaime
APPLICANT: Escobedo, Jaime
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION NUMBER: US/09/371,728
CURRENT APPLICATION NUMBER: US/09/371,728
CURRENT FILING DATE: 1999-08-10
FRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-01-08
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOCTWARE: Patentin version 3.0
EDNOTH: 36
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APPLICANT: Standboomb, Dan
APPLICANT: Estinchcomb, Dan
APPLICANT: Estinchcomb, Dan
APPLICANT: Estinchcomb, Dan
APPLICANT: Bacobedo, Jaime
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00, 876-3 (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
PRIOR TPLING DATE: 1999-08-10
PRIOR PILING DATE: 1999-10-26
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US-09-371-7728-12724
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Pred. No. 2.4e+03;
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Best Local Similarity 73.7%; Pred. No. 2.4e
Matches 14; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12724, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
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APPLICANT: Ribozyme Pharmaceuticals, Inc. APPLICANT: Pavco, Pam
  US/07/826,657
                                                                                                                                                                                                                                                                                                                                     1 CAGCGGAGTGATGGCAAGCACGAC 24
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APPLICATION NUMBER: US/07/8
FILING DATE: 21-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 392,679
FILING DATE: 11-AUG-1989
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US-09-371-772B-12724
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APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Becobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions .
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MHBB00,876-J (237/198)
CURRENT FILING DATE: 1999-08-10
PRIOR PILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-01-08
NUMBER OF SEQ ID NOS: 14225
SEQ ID NO 12890
LENGTH: 36
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Levels of Vascular Endothelial Growth Factor Receptor
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59.2%; Score 14.2; DB 3; Length 36;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 2; Mismatches 3; Indels
                                       FILE REFERENCE: MBHBOO, 876-J (237/198)
CURRENT APPLICATION WUMBER: US/69/371,772B
CURRENT APPLICATION WUMBER: US 60/005,974
PRIOR APPLICATION WUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
SEQ ID NO 12861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
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; Sequence 12890, Application US/09371772B
; Patent No. 6566127
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Best Local Similarity
Matches 14; Conserva'
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; Sequence 12819, Application US/09371772B
; Sequence 12819, Application US/09371772B
; Sequence 12819, Application
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: Pavco, Pam
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REPERENCE: MSHB00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US 60/005, 974
PRIOR PILING DATE: 1996-008-10
; PRIOR FILING DATE: 1996-01-08
; SOFTWARE: PatentIn Version 3.0
; SEQ ID NO 12819
; LENGTH: 36
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Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Scobedo, Jaime
APPLICANT: The Secobedo, Jaime
APPLICANT: The Secobedo Dan
APPLICANT: The Secobedo Dan
APPLICANT: The Secobedo Dan
APPLICANT: Stinchcomb Dan
APPLICANT: Stinc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 36;
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59.2%; Score 14.2; DB 3;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 2; Mismatches 3;
       CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR PTILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-09-371-772B-12861
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LENGTH: 36
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APPLICANT: ESCOBEGO, Jaimer Title OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R FILE REPERENCE: MBHB00, 876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,72B
CURRENT APPLICATION NUMBER: US/09/371,72B
RIOR PRILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-10-26
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12978
LENGTH: 36
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        Ribozyme Pharmaceuticals, Inc.
Pavco, Pam
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ORGANISM: Artificial Sequence
FEATURE:
                                                           McSwiggen, Jim
                                                                                          Stinchcomb,
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Sequence 12862. Application US/09371772B

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwigen, Jim
APPLICANT: McSwigen, Jim
APPLICANT: Escobedo, Jaine
TITLE OF INVENTION: Levels of Vacual Endothelial Growth Factor Receptor
FILE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
FILE REFERENCE: MBHB00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,72B
CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1999-08-10
PRIOR PILING DATE: 1999-08-10
PRIOR FILING DATE: 1996-01-08
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE PACENTION VALUED
SEQ ID NO 12962
LENGTH: 36
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TILE REFERENCE: MBHB00,876-J (237/198)
CURRENT APPLICATION WUMBER: US/09/371,772B
CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1999-08-10
PRIOR FILING DATE: 1995-01-26
RIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-7728-12939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 59.2%; Score 14.2; DB 3; Length 36; Best Local Similarity 73.7%; Pred. No. 2.46+03; Matches 14; Conservative 2; Mismatches 3; Indels
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Matches 14; Conservative
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LENGTH: 36
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Length 36; 3; Indels

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Run on:

Sequence:

Searched:

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BH863111 SALK 0931
BH863151 SALK 0932
CC039454 3591 10
BH891758 3526 119
AJ600111 Arabidops
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AZ8726 HM0145C20
AZ87375 G03617-3P
BZ384414 SALK 1355
AZ0013 MUB muscu
AU103111 AU103122
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Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by Sf.RACE of total RNA from gene trap ES
sequence tag generated by S.RACE of total RNA from gene trap ES
cell line. BS cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
CELL_LINE&KEY=XN495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC326423 50 bp mRNA linear GSS 16-MAY-2003 XN495 BayGenomics Gene Trap Library pGT2Lxf Mus musculus cDNA, mRNA sequence. CC326423
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Mus musculus
Musculus
Musculus
Muharycus; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/organism="Mus musculus"
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AJ600111
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Unpublished (2001)
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                                                            Query Match
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COMMENT
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AUTHORS
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CF331176 MACL--O7-
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                                                                                                                                              December 13, 2005, 12:51:49; Search time 2984 Seconds (without alignments) 376.304 Million cell updates/sec
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                         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Match Length DB
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Result

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/done_lbe="Gm-c1008"
/note="Wector: pSPORT1; Site_1: SalI; Site_2: NotI; This cond liberay was constructed from mRNA isolated from whole young pode, approximately 2cm long, of 12-week-old greenhouse grown plants. The library was prepared using the Life Technologies pSuperscript conha library construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a NotI restriction site. SalI linkers adapters were ligated to the blunt-ended cDNA fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-SalI restriction site of the pSPORTI vector. The ligated cDNA fragments were transformed into E. coli Electromax DH10B host cells. This library was constructed by Dr. Lila Vodkin and Dr. Anu Khanna."
                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. Putative full
length read vector to vector length is 50 This clone is available
through: Blogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA
(phone: 800 423 4163; email: info@biogeneticservices.com)
Insert Length: 2346 Std Brror: 0.00
Seq primer: -40RP from Glabco.
Location/Qualifiers
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, lamiids, Lamiales, Plantaginaceae, Antirrhineae,
       Shin, T., Jackson, Y., Cardenas, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H., Saedler,H. and Zachgo,S.
Saedler,H. and Zachgo,S.
Characterization of Antirrhium Petal Development and
Identification of Target Genes of the Class B MADS Box Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                           Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1008-874"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.7%; Score 13.6; DB 1; Length 49; llarity 80.0%; Pred. No. 1.6e+05; Conservative 0; Mismatches 4; Indels
Schurk, R., Ritter, E., Kohn, S., Shin, T. McCann, R., Waterston, R. and Wilson, R. Public Soybean EST Project Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant Cell 16 (12), 3197-3215 (2004)
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/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antirrhinum majus (snapdragon)
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Matches 16;
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                                                                                                                   CV933697 31 bp mRNA linear EST 25-JAN-2005 PMrpcm 3637 mating of 88069 (A1) and 618 (A2) Phytophthora infestans cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6d62bOS.yl Gm-c1008 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1008-874 5', mRNA sequence.
AW100845.1 GI:6071458
                                                                                                                                                                                                                                                                                                                                                                         l (bases I to 31)
Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
Kelkar,H., Fong,A.M., Gates,K., Roberts,S., Yatzkan,E., Gaffney,T.,
Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,
Windass,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,
Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
Lam,S.T. and Judelson, H.S.
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Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Large-scale gene discovery in the oomycete Phytophthora infestans reveals likely components of phytopathogenicity shared with true
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Phytophthora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Phytophthora infestans"
/mol_type="mkNa"
/mol_type="mkNa"
/db_xref="taxon:4787"
/sex="hal and A2"
/cone lib="mating of 88069 (A1) and 618 (A2)"
/note="Vector: pSPORT1"
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15782637
                                                                                                                                                                                                                                                                           Phytophthora infestans (potato late blight agent) Phytophthora infestans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Plant Pathology
University of California
Webber Hall, Riverside, CA 92521, USA
Tel: 909 787 4199
Fax: 909 787 4294
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Location/Qualifiers
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                                                                                                                                                                                                 CV933697
CV933697.1 GI:58123312
  28 CCGAGTGATGCCCAGCAGGA
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Best Local Similarity 80.v.
Best Local 6; Conservative
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Glires; Rodentia;
Muscapathi; Murcidea; Muridae; Murinae; Mus.
1 (bases 1 to 46)
Marra, M. Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Leo, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, P., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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ua91a06.rl Soares mammary gland NDMMG Mus musculus cDNA clone
IMAGE:1364818 5' Fimilar to SW:HBP HUMAN Q00341 HIGH DENSITY
LIPOPROTEIN BINDING PROTEIN ;, mRNA sequence.
                                                                              AVB39593 Nori Satoh unpublished cDNA library, young adult Ciona intestinalis cDNA clone rciad06£24, mRNA sequence.
                                                                                                                                                                                                                Ciona intestinalis
Ciona intestinalis
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Pulebobranchia; Cionidae; Ciona.
1 (bases 1 to 40)
Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
Expressed genes in Ciona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="whole animal"
/dev_stage="young adult"
/clone_lib="Nori Satoh unpublished cDNA library, young
adult"
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Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satch@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            th 54.2%; Score 13; DB 1; I Similarity 66.7%; Pred. No. 2.9e+05; 16; Conservative 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Ciona intestinalis"
|mol type="mkNA"
|db xref="texon:719"
|clone="rciad06f24"
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AV839593
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/mol type="mRNA"
/cultivar="Wackdong"
/db_xref="taxon:39947"
/clone="NACL-07-D03"
/tissue_type="callus"
/tissue_type="callus"
/dev stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_l: BcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group)

SM Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.

E (bases 1 to 40)

S Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song, S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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Pred. No. 2.4e+05;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                      Query Match 55.8%; Score 13.4; DB 1; Length 42; Best Local Similarity 73.9%; Pred. No. 1.9e+05; Matches 17; Conservative 0; Mismatches 6; Indels
                                                                                                                                                         /organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:151"
/clone="018 3 07 e21"
/tissue type="whole plant"
/clone_lib="Antirrhinum majus whole plant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Schwarz-Sommer Z
Molekulare Pflanzengenetik
MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Best Local Similarity
Matches 15; Conserv
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CF331176
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CF331176/c
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AZ776950
2M0011H04F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0011H04 F, genomic survey sequence.
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was hydrodynamically sheared by repeated passage through a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi, Muroidea, Muridae, Murinae, Mus. 1 (Bases 1 to 33)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Roilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCNH library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                    /clone_lib="KBrH, Brassica rapa HindIII BAC library GF-SCF-1002, Vector: pCUGIBac1" /lab_host="E.coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 28;
                                                                                         /organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/strain="chiftu type 401-42"
/cultivar="Chiftu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.3%; Score 12.8; DB 11; 70.8%; Pred. No. 3.5e+05;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0011 row: H column: 04
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                          /sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrH128N12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/clone="UUGC2M0011H04"
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Location/Qualifiers
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Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LILLIUDE SENDINA LINEAR GSS 09-AUG-2005 KBrH128N12 genomic clone, KBrH (HindIII) BAC library Brassica rapa Eubsp. pekinensis, genomic survey sequence.
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Contact: Bernd Weisshaar
Contact: Bernd Weisshaar
Belefeld University, Institute for Genome Research
Universitaetsstrasse 25, D-33594 Bielefeld, Germany Email:
bernd.weisshaar@uni-bielefeld.de
Bernd.weisshaar@uni-bielefeld.de
Bernd.weisshaar@uni-bielefeld.de
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Brassica rapa subsp. pekinensis
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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Li,Y. and Weisshaar,B.
Direct Submission
Submitted (09-AUG-2005) Weisshaar B., Bielefeld University,
Institute for Genome Research, Universitaetsstrasse 25, D-33594
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:8998038
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                                                                                                                                              Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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BAC end sequences of Brassica rapa
Unpublished
                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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clone="IMAGE:1364818"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sex="male"
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Best Local Similarity 76.23
Matches 16; Conservative
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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (14.NOV-2002) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
humquery@sanger.ac.uk Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSS 22-NOV-2002
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1 (bases 1 to 49)
Humphray, S. J., Huckle, E. and Hunt, S. E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence was generated from the SP6 end of BAC 49P1. 49P1 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
was hydrodynamically sheared by repeated passage through
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Danio rerio genomic clone DKEY-49P1, genomic survey sequence.
AL981974
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Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 12.8; DB 9; Length 49; Pred. No. 3.7e+05;
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-49P1"
/tissue_type="Testis"
/note="vector pindigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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Best Local Similarity 87.5%;
Matches 14; Conservative
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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|RF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-GGold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2M0136B09R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0136B09 R, genomic survey sequence.
AZ840176
AZ840176.1 GI:13010084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Boirognaphia; Eutheria; Euarchontoglires; Glires; Rodentia; Solurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 49)

Dunn, D., Aoyagi, A., Barber M., Beacorn, T., Duval, B., Hamil, C., Railly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Die genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="Male"
/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                                                                                                                                                                                                                                                                                                   53.3%; Score 12.8; DB 9; Length 33; 87.5%; Pred. No. 3.5e+05; tive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: C
Plate: 0136 row. B column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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'strain="CS7BL/6J"
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clone="UUGC2M0136B09"
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Location/Qualifiers
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Mus musculus
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Matches 14; Conservative
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Fax: 801 585 7177
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Best Local Similarity 87.5%,
Conservative
The Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Suzuki, Suzuki, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki, Jana.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
Institute of Suzuki, Suz
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                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                              Hominidae, Homo.

1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
EMBO Rep. 2 (5), 388-393 (2001)
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Mammalla; Butheria; Buarchontoglires; Primates; Catarrhini;
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1 (Dases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Suzuki, Y., Taira, H., Tsunoda, T., Morishita, S., Okubo, K.,

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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/organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/clone="HRC07124"
/clone="HRC07124"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50;
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   AU104990.1 GI:13554511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Yutaka Suzuki
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                                                              Homo sapiens (human)
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Homo sapiens
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Best Local Similarity
                                                                                          Homo sapiens
                           KEYWORDS
SOURCE
ORGANISM
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AU104991
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VERSION
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PCS01597X5 Scarlet Runner Bean Suspensor Region TriplEx2 Phaseolus coccineus CDNA 5' similar to sal85c10.y1 Gm-c1063 Glycine max cDNA, CA913527.1 G1:27400519
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                                                                                                                                                                                                                                                                                                                                                                                                                                             50 bp mRNA linear EST 28-JAN-2004
AU104992 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC1171, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzuki@ins.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
1-ength-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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(Dases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA stark sites

EMBO Rep. 2 (5), 388-393 (2001)
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                                                                        /clone_"HRC09125"
/clone_lib="Sugano Homo sapiens cDNA library"
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Pred. No. 3.7e+05;
0; Mismatches 2;
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Rammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Murcidae; Muridae; Musinae; Mus.

1 (bases 1 to 23)

S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid innerts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Diversity of Utah

Diversity of Utah

Diversity of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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2M0098H06F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0098H06 F, genomic survey sequence.
                                                                                                                              Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical
Science, University of Tokyo
Institute of Medical
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo.Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO rep. 2 (5), 388-393 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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/db_xref="texaon:9606"
/db_xref="texaon:9606"
/clone="zRV6C413"
/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: Plate: 0098 row: H column: 06
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Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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Location/Qualifiers
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AZ823791.1 GI:12993699
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Best Local Similarity
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AUTHORS
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COMMENT
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KEYWORDS
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                                                                                        JOURNAL
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                                         TITLE
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/dev_stage="6-days post-pollination"
/dov_stage="6-days post-pollination"
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/clone lib="Scarlet Runner Bean Suspensor TriplEx2"
/note="Organ: Suspensor Region of Globular-Stage Embryos;
/vector: TriplEx2; Site_1: SfilA; Site_2: SfilB; Suspensor
regions were micro-dissected from globular-stage embryos
six days after pollination from greenhouse-grown plants
[Weterings et al., Plant Cell 13, 2409-2425 (2001)].
Double-stranded cDNA was synthesized from suspensor mRNA
using the SMART cDNA Library Construction Kit according to
the manufacturer (Clontech). The suspensor cDNA fragments
were directionally ligated into the Sfil restriction site
of the lambda TriplEx2 vector (Clontech), and the
recombinant cDNAS were transformed into E. coli XLI-Blue
cells (Clontech). Suspensor cDNA plasmids used for
directional sequencing were obtained by in vivo excision
from the lambda TriplEx2 recombinants in E. coli BM25.8
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                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                  Department of Molecular, Cell, & Developmental Biology
University of California, Los Angeles
621 Charles E. Young Drive South, Los Angeles, CA 90095-1606, USA
Tel: 310 825 3270
Pax: 310 825 8201
                                                                                                                                                                                             1 (bases 1 to 42)

Weterings, K., Bi,Y.-P., Choi,J.-S.,
McBlroy, K.E., Choi,P.S., Harada,J.J., Fischer, R.L. and
Goldberg, R.B.
Gene Activity in Different Regions of a Post-Fertilization Plant
Embryo by EST Analysis
Unpublished (2002)
Contact: Goldberg, R.B.
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Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Phaseolus coccineus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 12.6; DB 6;
Pred. No. 4.5e+05;
0; Mismatches 4;
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AU108033
AU108033.1 GI:13557555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: bobg@ucla.edu
Seg primer: 5' TriplEx
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Phaseolus coccineus
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nes 15; Conserv
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Location/Qualifiers
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                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orfifice at constant velocity. The sheared DNA was blunt end repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114[gb]AP125072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-G304 (Stratagene) cells and selected for ampicillin resistance."
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When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. Trace
considered overall poor quality Possible reversed clone: similarity
on wrong strand This clone is available through: Biogenetic
Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423
Seq primer: -40UP from Gibco
POLYA-NO.
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Shoemaker, R., Kehim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Shoemaker, R., Kehim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Undarra, M., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
McCani, R., Waterston, R., and Wilson, R., Jackson, Y., Cardenas, M.,
Public Soybean EST Project
Unpublished (1999)
Public Soybean EST Project
Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
           /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note=""vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/65 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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AUTHORS
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JOURNAL
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BF347447 37 bp mRNA linear EST 22-NOV-2000
6020020355F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156238
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bumaniai; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1 (bases 1 to 37)
NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
                                           /db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1004-783"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.7%; Score 12.4; DB 1; Length 31; larity 72.7%; Pred. No. 5.3e+05; Conservative 0; Mismatches 6; Indels
organism="Glycine max"
                                                                            /tissue_type="root"
/lab_host="XL10-Gold"
                /mol_type="mRNA"
/cultivar="Williams"
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Gaps

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GSS 29-APR-2005
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus, Xenopus
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33 bp DNA linear GSS 29-APR-20 d01430-3prime Exelixis P element XP insertions Drosophila melanogaster genomic Squence recovered from 3' end of P element, genomic survey sequence.
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The information of this clone is available through the following
URL.
units. For more information on RescueMu, go to the wet site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB
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/dev_stage="stage 15"
/clone_lib="NIBB Mochii normalized Xenopus neurula
library:
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Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Pred. No. 6.6e+05;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                      44;
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laevis cDNA clone XL019f12 5', mRNA sequence.
BJ032969
BJ032969.1 GI:17391810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expressed genes in X. laevis embryo Unpublished (2001)
Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics Institute Institute of Genetics Institute of Genetics Institute Institute
                                                                                                                                                                                                                                                                             S1.7%; Score 12.4; DB 9;
ilarity 72.7%; Pred. No. 5.6e+05;
Conservative 0; Mismatches 6;
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                                                                                                                                                                                         plates with ampicillin.
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/db_xref="taxon:8355"
/clone="XL019f12"
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Location/Qualifiers
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Contact: Malbot V
Department of Biological Sciences
Stanford University
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1007061G07.2EL_y1 1007 - RescueMu Grid H Zea mays genomic, genomic
Burvey sequence.
BH620252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="1007 - RescueMu Grid H"
/clone lib="1007 - RescueMu Grid H"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site_2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1007061 column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                          /lob host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Brn67"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dr. Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4156238"
/tissue_type="anaplastic oligodendroglioma with 1p/19g
                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM9428 row: n column: 15
High quality sequence stop: 37.
Location/Qualifiers
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/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.7%; Score 12.4; DB 2; 72.7%; Pred. No. 5.5e+05; ive 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     855 California Ave, Palo Alto, CA 94304,
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                   organism="Homo sapiens"
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/organism="Zea mays"
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/dev_stage="adult"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 AGTGCTGGGATTACAAGCACGA 14
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nes 16; Conserv
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LOCUS
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Matches
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Gaps

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Hordeum vulgare subsp. vulgare
bkaryvota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
Pooideae; Triticage; Hordeum.
1 (bases 1 to 38)
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38 bp DNA linear GSS 16-FEB-200
IMOS84PO1R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Sciurcognathi, Murcidea, Muridae, Murinae, Mus.

1 (bases 1 to 38)
Dunn,D., Aoyadi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Miederhausern,A. and Wright,D., Weiss,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                 Barley EST sequencing project in NIG and Okayama Univ Unpublished (2001)
Contact: Kazuliro Sato
Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Bmail: kazasto@rib.okayama-u.ac.jp,
URL:http://www.rib.okayama-u.ac.jp,
Sato, K., Saisho, D., Takeda, K., Shini, T. and Kohara, Y. Direct submission;
                                                                                                                                                                                                                                                                                                                                                                                                          database:http://www.shigen.nig.ac.jp/barley/Barley.html.
Location/Qualifiers
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/organism="Hordeum vulgare subsp. vulgare"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.0
Plate: 0584 row: P column: 01
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/cultivar="Haruna Nijo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sub_species="vulgare"
/db_xref="taxon:112509"
/clone="bags11124"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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AZ773196/c
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TITLE
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                                                             Drosophila melanogaster (fruit fly)

Brosophila melanogaster

Eukaryota, Merezoa, Arthropoda; Hexapoda; Insecta; Pterygota;

Eukaryota, Drosophilae;

Baphydroidea; Drosophilae;

Ephydroidea; Drosophilae;

Ephydroidea; Drosophilae;

Ephydroidea; Drosophilae;

Ephydroidea; Drosophilae;

Enthault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A.,

Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L.,

Greer,K., Hartouni,S.R., Howie,E., Jakkula,L., Joo,D., Killpack,K.,

Laufer,A., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C.,

Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F.,

Swimmer,C., Kopczynski,C., Duyk,G., Winberg,M.L. and Margolis,J.

A complementary transposon tool kit for Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .33
/organism="Drosophila melanogaster"
/organism="Trosophila melanogaster"
/mol_type="genomic DNA"
/strain="isogenic w- strain"
/db xref="taxon:722"
/clone lib="Excalixis P element XP insertions"
/clone lib="Excalixis P element XP (GenBank accession number AY515149); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. For the P element XP, we selected an easily mobilized ammunition element Among inserts hopped onto the Binsinscy balancer. New insertions were collected in vials from dysgenic females using the standard chromosomal source of transposaes, delta2-3. All lines were mapped to homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: Rhoskins@lbl.gov
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P
Sequence orientation is forward strand relative to 5' end of P
The P element insertion position is 1 in the 33 bases. This
insertion position refers to the first base of the 8 base target
recognition sequence.
Class: transposon insertion site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-112, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
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                                                                                                                                                                                                                                                                                                                                                                                                     using P and piggyBac Nat. Genet. 36 (3), 283-287 (2004) 14981521
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Hordeum vulgare subsp. vulgare
CZ472229
CZ472229.1 GI:62966242
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Sanderson, S.I., Finlayson, H.A. and Archibald, A.L.

Randerson, S.I., Finlayson, H.A. and Archibald, A.L.

Development of CDNA and EST resources for studying reproduction and embryo development in pigs and cattle

Unpublished (2004)

Contact: Anderson SI

Genomics and Bioinformatics

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with the -minscore 20

and -minmatch I2 options. Vector: PBlueSGriptII(KS+) R. Site 1:

ECORI R. Site 2: NotI Description: Normalised library constructed

from pooled tissue from day 30 placentes. Clones available from UK

Centre for Functional Genomics in Farm Animals, Roslin Institite,

Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
                                                                                                                                                                                                                                                                                                                               /mol type="genomic DNA"
/facin-isogenic w. strain"
/db_xref="taxon:722"
/db_xref="taxon:722"
/clone lib="taxon:722"
/clone lib="sxelixis P element XP insertions"
/note="vector: P element XP (GenBank accession number AY515149); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable welements. For the P element XP, we selected an easily mobilized ammunition element among inserts hopped onto the Binsinscy balancer. New insertions were collected in vials from dysgenic females using the standard chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source of transposase, delta2-3. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                        The P element insertion position is 31 in the 38 bases. This insertion position refers to the first base of the 8 base target recognition sequence.
                               Sequence recovery method was inverse PCR. Sequence orientation is forward strand relative to 5' end of {\tt P}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                         /organism="Drosophila melanogaster"
                                                                                                                                                                                                                Class: transposon insertion site.
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/db_xref="taxon:9823"
/clone="C0000048_C19"
                                                                                                                                                                                                                                             Location/Qualifiers
Email: RHoskins@lbl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AJ669015.1 GI:49353469
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Sus scrofa
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AJ669015
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Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

E 1 (bases 1 to 38)

Inbault, S. T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A., Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L., Ryner, L., Cheung, L.M., Chong, A., Brickson, C., Fisher, W. W., Greer, K., Hartouni, S.R., Howie, E., Jakkula, L., Joo, D., Killpack, K., Laufer, A., Mazzotta, J., Smith, R.D., Stewns, L.M., Stuber, C., Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, F., Swimmer, C., Kopczynski, C., Duyk, G., Winberg, M.L. and Margolis, J. A. Complementary transposon tool kit for Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                           Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared bNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                         /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"/clone_lib="Mouse_10kb plasmid UUGClM library."
/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
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14981521
                                                                                              'organism="Mus musculus"
                                                                                                                        /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0584P01"
   High quality sequence stop: 38.
Location/Qualifiers
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                                                                                                                                                                                                                                                   sex="Male"
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BH863111 42 bp DNA linear GSS 05-AUG-2002 SALK 093187 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_093187, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="SAIK 091178"
/clone="SAIK 091178"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
threctly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Frednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R. A Sequence-Indexed Library of Insertion Mutations in the
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A Sequence-Indexed Library of Insertion Mutations in the
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                                                                                                                                                                                                                                                                                                           This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At2g10530. Class: TDNA tagged. Location/Qualifiers
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
TH: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                          Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Email: ecker@salk.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 50.0%; Score 12; DB 9; Length 42; Local Similarity 75.0%; Pred. No. 8.5e+05; Local 15; Conservative 0; Mismatches 5; Indels
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col.0"
/db_xref="taxon:3702"
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Unpublished (2001)
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Arabidopsis thaliana
Busaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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I (basea 1 to 47)
Satoh, N., Satoh, Y., Kohara, Y. and Shin-i, T.
Expressed genes in Ciona intestinalis
Contact: Nori Satoh
Department of Zoology
         /clone_lib="CSEQRANO9"
/note="Vector: pBlueScriptII(KS+); Site_1: BcoR1; Site_2:
Not1; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."
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/dev stage="young adult"
/clone_lib="Nori Satoh unpublished cDNA library, young
adult"
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                                                                                                                                                   Length 44;
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                                                                                                                                                 50.8%; Score 12.2; DB 1;
82.4%; Pred. No. 6.9e+05;
tive 0; Mismatches 3;
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
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/db_xref="taxon:7719"
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Alonso, J. M., Leisse, T. J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C. J., Parker, H., Prednis, L., Shinh, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Conteat: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute Genomic Analysis Laboratory (Institute Genomic Analysis Laboratory (Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ902826
K071087-T7 Library RPCI1,3-5 Human PAC Homo sapiens genomic clone RPCIP704K071087, genomic survey sequence.
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TDNA insertion lines Arabidopsis
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/clone="SALK 093383"
/clone="SALK 093383"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the aite of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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Location/Qualifiers
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.larity 75.0%; Pred. No. 8.5e+05;
Conservative 0; Mismatches 5; Indels
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/mol_type="genomic DNA"
/ecotype="Col-0"
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/clone="SALK 093187"
/clone="SALK 093187"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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/clone="SALK 093195"
/clone="lb="Arabidopsis thaliana TDNA insertion lines"
/clone lib="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At2g10530.
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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   'organism="Arabidopsis thaliana"
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                                   /mol_type="genomic DNA"
/ecotype="Col-0"
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/ecotype="Col-0"
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Location/Qualifiers
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Best Local Similarity 75.0
Matches 15, Conservative
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BH863117
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Gaps

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pBlueScript backbone); Site 1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid P was grown at Molokai in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH108 cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Contact: Walbor (2001)
Contact: Walbor (2001)
Contact: Walbor (2001)
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 227
Fax: 650 725 8221
Email: walbor defanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 352_119_1 row: 29
Class: transposon-tagged.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /moi type="mixed background W23/A188/B73"
/moi type="mixed background W23/A188/B73"
/db ref="taxon:4577"
/tissue_type="leaf"
/de-stage="adult"
/deb host="wlh103"
/lab host="wlh103"
/lote="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHi; Site_2: BglII; RescueMu is a 4.9 kb, modifide maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transposon unite: For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid K was grown at Molokai, Hawaii in Winter 2000-2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and liqated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bp DNA linear GSS 14-AUG-2002
- RescueMu Grid K Zea mays genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
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75.0%; Pred. No. ...
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genomic survey sequence.
BH8977a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCGGAGTGATGGCAAGCAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 AGCCGGGGGGTGGCCAGCAC 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:22222805
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Best Local Similarity 75...
Best Local Similarity
For 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 49)
Walbot, V.
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ВН891758.1
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                       A hexander.C., Bernstein,S.L., Rocchi,M. and Auburger,G.
Salvarader.C., Bernstein,S.L., Rocchi,M. and Auburger,G.
Saturating Density of STSs (1/6 kb) in a 1.1 Mb Region on 3q28-q29:
A Valuable Resource for Cloning of Disease Genes
L Unpublished (2000)
Contact: Alexander C
Department of Molecular Genetics
Institute of Ophthalmology, University College London
11-43 Bath Street, London EC1V9EL, UK
Tel: +44 171 608 6833
Fax: +44 171 608 6833
Email: calexand@hgmp.mrc.ac.uk
Seq primer: 'nested' T7-Primer cggtcgagcttgacattgtag
Class: PAC end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCU39454 47 bp DNA linear GSS 01-APR-2003
3591 1 104 1 E12.1EL x 2 3591 - RescueMu Grid P Zea mays genomic,
genomic survey sequence.
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1 (bases 1 to 47)
Walbot,V.
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Contact: Walbot V
Department of Biological Sciences
Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     855 Galifornia Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8227
Enail: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Neverse complemented post-ligation sequence from source sequence.
Plate: 3591_104_1 row: 17
Class: transposon-tagged.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="RPCIP704K071087"
/clone lib="Library RPCI1,3-5 Human PAC"
/note="Human genomic PAC library RPCI (loannou et al.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Zea mays"
/mol type="genomic DNA"
/mol type="genomic DNA"
/mol type="genomic DNA"
/cissue_type="leaf"
/db xref="Lexon:4577"
/tissue_type="leaf"
/dev stage="adult"
/lab-bost="BH10B"
/clone_lib="3591 - RescueMu Grid P"
/note="Organ: leaf; Vector: RescueMu (engineered from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                      cocation/Qualifiers
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SM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Nooptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Nooptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
E 1 (bases 1 to 30)
S Thibault,S.T.; Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A., Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L., Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W., Greer,K., Hartouni,S.R., Howie,E., Jakkula,L., Joo,D., Killpack,K., Laufer,R., Mazotta,J., Smith,R.D., Stevens,L.M., Stuber,C., Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zahao,L., Chen,F., Swimmer,C., Kopczynski,C., Duyk,G., Winberg,M.L. and Margolis,J. A complementary transposon tool kit for Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 bp DNA linear GSS 29-APR-2005 d04146-3prime Exelixis P element XP insertions Drosophila melanogaster genomic Sequence recovered from 3' end of P element, genomic survey sequence. C2473756 CZ473756.1 GI:62967769
                                                                                                                                      Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Scienconathi; Muroidea; Murinae; Mus.

1 (bases 1 to 50)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Bogers, J., and Bradley, A.

Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The P element insertion position is 1 in the 30 bases. This insertion position refers to the first base of the 8 base target recognition sequence.
chromosome engineering clone MHPP182e10, genomic survey sequence.
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Sequence orientation is forward strand relative to 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Email: RHoskins@lbl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.0%; Score 12; DB 11; Length 50
75.0%; Pred. No. 8.7e+05;
tive 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPP182e10"
/clone_lib="MHPP"
                                                                      GSS; genome survey sequence;
Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 GGATTAAAGGCATGCACCAC 13
                         CR086418
CR086418.1 GI:49820010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Conservative
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CZ473756/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (13-00T-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante.info.infoblogen.fr).
                                                                                                                                                                                                                                                       Arabidopsis thaliana T-DNA flanking sequence, right border, clone 50009, genomic survey sequence.
AJ60011.1 GI:37949739
GSS; right border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Craudd, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                                                                              Gaps
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                              Length 49;
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/mol type="genomic DNA"
/db_xref="taxon:3702"
/clone="500C09"
                              Score 12; DB 9; I
Pred. No. 8.7e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="T-DNA flanking sequence
            50.0%; Scor. 75.0%; Pred. No. e...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'ecotype="Wassilewskija"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CAGCGGAGTGATGGCAAGCA 20
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                                                                                                                           2 AGCGGAGTGATGGCAAGCAC 21
                                                                                                                                                                         26 AGCGGAGAGAGAGCTAGCCC 45
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Balzergue, S.
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Matches 15; Conservative
                                                                              15; Conservative
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                                             Best Local Similarity
Matches 15; Congery
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                                Query Match
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CR086418/c
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DEFINITION
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AUTHORS
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JOURNAL
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Gaps

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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources from from the Jackson
(http://www.jax.org/resources/documents/dhares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1M0145C20R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0145C20 R, genomic survey sequence.
AZ386728
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1 (bases 1 to 41)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
49.2%; Score 11.8; DB 9; Length 4
Best Local Similarity 69.6%; Pred. No. 1e+06;
Matches 16; Conservative 0; Mismatches 7; Indels
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Insert Length: 1000 Std Error:
Plate: 0145 row: C column: 20
Seg primer: CACACAGAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0145C20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 41.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ386728.1 GI:10500428
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Fax: 801 585 7177
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KEYWORDS
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AZ386728/c
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                                                                                         /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="stage="genomic DNA"
/strain="stage="genomic DNA"
/db xref="taxon:722"
/clone lib="Exelixis P element XP insertions"
/clone lib="Exelixis P element XP (GenBank accession number Note="Vector: P element XP (GenBank accession number AY515149); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. For the P element XP, we selected an easily mobilized ammunition element among inserts hopped onto the Binsinscy balancer. New insertions were collected in vials from dysgenic females using the standard chromosomal source of transposase, deltaz-3. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."
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2M0093G24R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0093G24 R, genomic survey sequence.
AZ821223
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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1 (bases I to 40)
1 Lislam, H., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
1 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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Insert Length: 10000 Std Error: 0.00
Plate: 0093 row: G column: 24
Seg primer: CACACAGGAAACAGCTAATGACC
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                              Class: transposon insertion site.
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/clone="UUGC2M0093G24"
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Location/Qualifiers
                                                  Location/Qualifiers
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Mus musculus
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Fax: 801 585 7177
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AZ821223/c
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E., SLC,

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49.2%; Score 11.8; DB 1; Length 43; 69.6%; Pred. No. 1e+06; 1ive 0; Mismatches 7; Indels
                /tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: December 13, 2005, 15:51:21 Job time: 2988 secs
/clone="IMAGE:2165334"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 AGAGGCTCGGCGCCAAGCAAGAC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AGCGGAGTGATGCCAAGCACGAC 24
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Matches 16; Conserva
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                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|qb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tm89g04.x1 NCI CGAP Brn25 Homo sapiens CDNA clone IMAGE:2165334 3' similar to SW:WASP_MOUSE P70315 WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bonaldo, Ph.D. cDN and by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                            /clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
  'lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
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NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRGAP), Tumor Gene Index
Unpublished (1998)
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                                                                                                           Laboratory Mouse DNA Resource
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/mol_type="mRNA"
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Abk20721 Human ERG
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Adm61863 Hepatitis
Adh85578 Anti huma
Adu85578 Human TER
Adu9468 Human TER
Adu94463 Human TER
Adm90361 Human PTP
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Adu94468 Human ChK
Abk05415 Human CCC
Abk59159 Human CLC
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Abk05395 Human NOG
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Abk05391 HBV G-cle
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ALIGNMENTS

ss; PCR; high altitude pulmonary edema; pulmonary edema; respiratory-gen.; respiratory disease; SNP detection; allelic variation; primer; exon. Human inducible nitric oxide synthase gene exon 7 forward PCR primer. Detecting predisposition to high altitude pulmonary edema (HAPE) by amplifying intron 7 of human inducible nitric oxide synthase gene, a predicting and analyzing differences in the distribution of allelic (COUN-) COUNCIL SCI & IND RES INDIA. BP. 13-NOV-2003; 2003US-00713137. 13-NOV-2003; 2003US-00713137. ADZ75765 standard; DNA; 24 (first entry) Pasha AQM, Ahsan A; WPI; 2005-384299/39. US2005106573-A1.

Claim 6; SEQ ID NO 2; 13pp; English.

The invention relates to a novel method for detecting predisposition to high altitude pulmonary edema (HAPE). The method comprises amplifying intron 7 of the human inducible nitric oxide synthase (NOS) gene (ADZ75764) by designing and synthesizing forward and reverse oligonucleotide primers (ADZ75765+ADZ75766), and predicting and

ABK05366 ADV47946

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CC DNAzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr an amberzyme (cleaving RNA thich an NGV motif). The CD20-targetting nucleic acid is used to cleave RNA with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg^2+. Furthermore, it may be contacted with a cell to reduce CD20 activity of the CD20. The treatment may further comprise the use of one or more of CD20. The treatment may further comprise the use of one or more cof therapies. In particular, the CD20 targetting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular NHL, lymphocytic treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular NHL, lymphocytic CC leukaemia, HTV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), samil B-cell lymphocytic lymphoma, immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), satcheropathy. The NOGO gene in the presence of a divalent cation that is preferably Mg^2+. Furthermore, the nucleic acid may be conteated with a cell to reduce NOGO activity of the coll and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more charapies. In particular, the NOGO-targetting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CNA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, muscular dystrophy, and/or other neurodegenerative disease catates which respond to the modulation of NOGO expression. The present sequence is a substrate sequence for a nucleic acid of the invention coll based on the human NOGO sequence for a nucleic acid of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid molecules, which downregulates expression of a checkpoint kinase-1 gene, useful for treating colorectal, lung, breast or prostate cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.8%; Score 18.2; DB 4; Length 37; 78.3%; Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 37 BP; 10 A; 8 C; 12 G; 0 T; 7 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mcswiggen J, Booher RN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.1e
2; Mismatches
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RNA cleavage; cancer; ss.
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AAH96727
                HANDER STATE OF THE STATE OF TH
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    statistically analyzing differences in the distribution of the allelic variants in the populations, where GG genotype at 19480 position are at low risk of HAPE, and AA genotype at 19480 position are at HAPE. The present sequence represents the forward oligonucleotide primer
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                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                     100.0%; Score 24; DB 14; Length 24; 100.0%; Pred. No. 0.18; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                Sequence 24 BP; 7 A; 6 C; 9 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CAGCGGAGTGATGGCAAGCACGAC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGCGGAGTGATGGCAAGCACGAC 24
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28-FEB-2000; 2000US-0185516P.
06-MAR-2000; 2000US-0187128P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                       the invention.
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WO200159103-A2.

16-AUG-2001.

Blatt L,

CHOM/) (MCSM/)

sapiens

Synthetic

12-MAR-2002

ABK05395;

RESULT 2 ABK05395

Query Match

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Best Local Similarity
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27-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADU94766;
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ADU94766
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                                   The present invention provides nucleic acid molecules capable of downregulating the expression of the human checkpoint kinase-1 (Chk1) depene. These may be antisense or ribozyme sequences, and are useful in the treatment of diseases associated with conditions affected by Chk1 levels, including cancer. The present sequence is an oligonucleotide described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                             Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase; hetaAP-2; human telomerases; hTERT; protein kinase C alpha; PKC alpha; beta-secretase; BACE; human epidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; PLN; preseniln-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver; amberzyme; zinzyme; DNAzyme; cancer; baraticis B virus; disease; disease; disease; disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
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                                                                                                                                            71.7%; Score 17.2; DB 4; Length 37; 77.3%; Pred. No. 3.1e+02; ive 2; Mismatches 3; Indels
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Matulic-Adamic J, Sweedler D, Draper K, Ch
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
                                                                                                                     Sequence 37 BP; 11 A; 6 C; 13 G; 0 T; 7 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                        Human PLN G-cleaver ribozyme sequence #9
                                                                                                                                                                                                           2 AGAGGAGUGAUGCACUA 23
                                                                                                                                                                                             2 AGCGGAGTGATGGCAAGCACGA 23
            Claim 5; Page 68; 115pp; English
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99US-00406643.
99US-015623P.
99US-0156430.
99US-00436430.
99US-0169100P.
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                                                                                                                                                       Local Similarity 77.3%;
hes 17; Conservative
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                                                                                                                                                                                                                                                                                                                                  10-FEB-2005 (first entry)
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Stinchcomb D,
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04-FEB-2000;
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                                                                                                                                              Query Match
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WPI; 2001-244406/25

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The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBR), protein kinase C alpha (PKC alpha), beta-secretaee (BACE), human epidermal growth factor receptor-2 (pse-2b2/neu), phospholamban (PLN), presenilin-1 (ps-1), presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-Claever, amberzyme, cinclude hammerhead (HH), hairpin, NCH (inozyme), G-Claever, amberzyme, cinclude hammerhead (HH), patiticular breast cancer, Alzheimer's disease, cor treating cancer, in particular breast cancer, Alzheimer's disease, dispensiv, cardiac diseases e.g. heart disease, as carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased calls and to detect the presence of specific RNA in a cell. The present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.
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Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 37 BP; 8 A; 6 C; 15 G; 0 T; 8 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human TERT G-cleaver ribozyme sequence #157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.
                                                                                                            Example 5; Page 428; 717pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCUGAGUGAUGCAUGCACUA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 AGCGGAGTGATGGCAAGCACGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0151713P.
99US-00406643.
99US-0156236P.
99US-0156467P.
99US-00436430.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADU94766 standard; RNA; 36 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-AUG-2000; 2000WO-US023998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                        obesity and heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-1999;
08-NOV-1999;
06-DEC-1999;
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The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBRT), protein kinase C alpha (PKC alpha), beta-secretase (BACB), human epidermal growth factor receptor-2 (HER2/c-erb2/neu), phospholamban (PLM), presentlin-1 (ps-1), presentlin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, zinzyme, and/or DNAzyme motifs. The methods of the invention are useful for treating cancer, in particular breast anacer, Altreimer's disease, diabetes, obesity, cardiac disease e.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells and to detect the presence of specific RNA in a cell. The present sequence represents a ribozyme used in the examples of the present incention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.
                                                                                                                                                                                                                                                                                                                                                                                           Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
                                                                                                                                                                                                                                                                           Chowrira B;
                                                                                                                                                                                                                                                   Jøman N, Blatt L, Beigelman L, Burgin A;
Aatulic-Adamic J, Sweedler D, Draper K, Ch
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 36 BP; 8 A; 10 C; 12 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 304; 717pp; English.
                                                                                                                                                                                                                                                 Blatt L,
                                                                                                                                                                                                                                                 Usman N, Blatt L,
Matulic-Adamic J,
                                                                                     20-MAR-2000; 2000US-00531025.
14-APR-2000; 2000US-0197769P.
23-MAY-2000; 2000US-00578223.
09-AUG-2000; 2000US-00636385.
                   99US-0173612P.
99US-00476387.
2000US-00498824.
                                                                                                                                                                                                      (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                        obesity and heart disease.
                                                                                                                                                                                                                                                                                                                                              WPI; 2001-244406/25
                                                                                                                                                                                                                                                                                                Stinchcomb D,
                                                                04-FEB-2000;
                                                                                                                                                                                                                                                 Mcswiggen J,
Karpeisky A,
                   29-DEC-1999;
30-DEC-1999;
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ö 0; Gaps Score 16.8; DB 5; Length 36; Pred. No. 4.8e+02; 2; Indels 2; Mismatches 70.0%; Query Match Best Local Similarity 80.0 Matches 16; Conservative

4 CGGAGTGATGGCAAGCACGA 23 cesasous de consecue de consec

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ABK05358 standard; RNA; 37 12-MAR-2002 ABK05358; RESULT 6 ABK05358

Human NOGO G-Cleaver substrate sequence #21. (first entry)

Human; 88; antiBense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; anotropic; neuroprotective; antiparkinsonian; muscular; D20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNAzyme; inOzyme; G-Cleaver; amberzyme; zinzyme; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphom; leukaemia; Human immunodeficiency virus; HTV associated MHL; mantle-cell lymphoma; MCL; immunocytoma; MC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury;

cerebrovascular accident, CVA, Alzheimer's disease, multiple sclerosis, chemcherapy-induced neuropathy, amyotrophic lateral sclerosis, ALS; Parkinson's disease, ataxia; Huntington's disease; substrate sequence; Creutzfeldt-Jakob disease; muscular dystrophy, neurodegenerative disease.

WO200159103-A2. sapiens 16-AUG-2001 Synthetic. Homo

09-FEB-2001; 2001WO-US004273

11-FEB-2000; 2000US-0181797P. 28-FEB-2000; 2000US-0185516P. 06-MAR-2000; 2000US-0187128P.

RIBOZYME PHARM INC. CHOWRIRA B M MCSWIGGEN J. BLATT L. (RIBO-) (CHOM/) (BLAT/) (MCSM/)

Chowrira BM; Blatt L, Mcswiggen J,

WPI; 2001-607195/69.

and Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, central nervous system injury.

Claim 89; Page 92; 200pp; English.

The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NGCO). The crequists may be enzymatic nucleic acids (e.g. a ribozyme or a nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a numberzyme (an endolytic nucleic acid cleaving a nn RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) proposessing an NCH motif). The CD20-targetting nucleic acid is used to cleaver RNA with a rYSY motif). The CD20-targetting nucleic acid is used to cleaver RNA cc C CD20 in the presence of a divalent cation that is preferably with the level cc CC CD20 in the presence of a divalent cation that is preferably of the ccl and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targetting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, leukaemia, MIV (human immunodeficiency virus) associated WIL, mantle-cell lymphoma (MLL), immunocycoma (TMC), small B-cell lymphomy. The NOGO targetting nucleic acid is used to cleave RNA of the NOGO gene in the nucleic acid may be contacted with a cell to reduce NOGO activity of the contact a patient having a condition associated with the level of the cate central nervous system (CNS) injury and cerebrowsscular accident (CNS), atroke), Alzhaimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, and/or other neurodegenerative disease trans, Huntington's disease, creates which respond to the modulation of content entered for a nucleic acid of the invention the server of the seases. Muscular descence for a nucleic acid may be received for a nucleic acid of the invention sequence is a substrate sequence based on the human NOGO sequence

Sequence 37 BP; 5 A; 10 C; 17 G; 0 T; 5 U; 0 Other;

Gaps .. 0 69.2%; Score 16.6; DB 4; Length 37; 73.9%; Pred. No. 6e+02; tive 2; Mismatches 4; Indels Conservative Best Local Similarity Matches 17; Conserv Query Match

Gaps

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Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-lb; PTB-1B; methionine aminopeptidase; hetaPa-2, human telomerase; hTERT; protein kinase C alpha; PKC alpha; beta-secretase; BACB; human epidermal growth factor receptor-2; HER2; e-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; innoxyme; G-cleaver; amberzyme; zinzyme; DNAzyme; Cancer; breast cancer; Alzheimer's disease; diabetes; obesity; cardiac disease; heart disease; agg-related disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
for treating cancer, in particular breast cancer, Alzheimer's disease, diabetes, obesity, cardiac diseases e.g. heart disease, age-related diseases, hepetitis B infections, and hepetitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells and to detect the presence of specific RNA in a call. The present sequence represents a ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Usman N, Blatt L, Beigelman L, Burgin A;
Matulic-Adamic J, Sweedler D, Draper K, Ch
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
                                                                                                                                                                                                                                                              Score 16.6; DB 5; Length 37; Pred. No. 6e+02; 2; Mismatches 4; Indels
                                                                                                                                                                                                                        Sequence 37 BP; 8 A; 10 C; 12 G; 0 T; 7 U; 0 Other;
                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human BACE G-cleaver ribozyme sequence #12.
                                                                                                                                                                                                                                                                                                                                                        CAGCGGAGTGATGGCAAGCACGA 23
                                                                                                                                                                                                                                                                                                                                                                                  99US-00406643.
99US-0156236P.
99US-0156467P.
99US-00436430.
99US-00474432.
99US-0173612P.
99US-00476387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0197769P
                                                                                                                                                                                                                                                                     69.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-AUG-2000; 2000WO-US023998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-00578223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADV04075 standard; RNA; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beaudry A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                               17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-244406/25.
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200116312-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stinchcomb D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mcswiggen J,
Karpeisky A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-DEC-1999;
29-DEC-1999;
29-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-FEB-2005
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08-NOV-1999;
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                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADV04075
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             8888888888888
                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                   Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase; hetherAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha; beta-secretase; BACE; human epidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inoxyme; G-cleaver; amberzyme; zinzyme; DNAzyme; cancer; baration; Alzheimer's disease; disease; chesity; cardiac disease; heart disease; age-related disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (FTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBRT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1), presenilin-2 (ps-2), and hepatitis B virus (HBN) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, zinzyme, and/or DNAzyme motifs. The methods of the invention are useful
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Matulic-Adamic J, Sweedler D, Draper K, Ch
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 6; Page 531; 717pp; English.
                                                                                                                                                                                                                                                                                                  HBV G-cleaver ribozyme sequence #57.
                                                       23
                 CAGCGGAGTGATGGCAAGCACGA 23
                                     CAGGGGGGGAGGCAUGCACUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0151713P.
99US-016643.
99US-0156236P.
99US-0156447P.
99US-0169100P.
99US-016100P.
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2000US-0197769P
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                                                                                                                                                                     ADV47962 standard; RNA; 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     obesity and heart disease.
                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis B virus.
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Karpeisky A, Mi
Stinchcomb D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200116312-A2.
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29-DEC-1999;
29-DEC-1999;
30-DEC-1999;
04-FEB-2000;
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08-NOV-1999
                                                                                                                                                                                                                                                       10-FEB-2005
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                                                                                                                                                                                                               ADV47962;
                                                                                                                             RESULT 7
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Chowrira

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The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of enes encoding protein-tyrosine-phosphatase-lb (PTB-1B), metholonine aninopeptidase (METAP-2), human Lelomerase (MTERT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (HERZ/C-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1), presenilin-1 (ps-1), presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), harrpin, NCH (inozyme), G-cleaver, amberzyme, include hammerhead (HH), harrpin, NCH (inozyme), G-cleaver, amberzyme, include hammerhead (HH), harrpin, NCH (inozyme), g-cleaver, amberzyme, cinzyme, and/or DNAzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Alzheimer's disease, disease, disease, hepatitis B infections, and hepatitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells and to detect the presence of specific RNA in a cell. The present sequence represents a ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.
Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 37 BP; 5 A; 9 C; 18 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                          Example 4; Page 364; 717pp; English.
                                                                                                                                     obesity and heart disease.
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Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.

B,

Chowrira

Usman N, Blatt L, Beigelman L, Burgin A; Matulic-Adamic J, Sweedler D, Draper K, Ch Beaudry A, Zinnen S, Lugwig J, Sproat BS;

Stinchcomb D, Beaudry A,

Mcswiggen J, Karpeisky A,

WPI; 2001-244406/25.

29-DEC-1999; 990S-0173612P.
30-DEC-1999; 990S-00476387.
04-FEB-2000; 2000US-0049824.
20-MAR-2000; 2000US-00531025.
14-APR-2000; 2000US-005769P.
23-MAY-2000; 2000US-005769P.

(RIBO-) RIBOZYME PHARM INC

99US-00474432 99US-0173612P

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                                                                                                                                                        69.2%; Score 16.6; DB 5; Length 37; 73.9%; Pred. No. 6e+02; ive 2; Mismatches 4; Indels
                                                                                                                                                                              1 CAGCGGAGTGATGGCAAGCACGA 23
                                                                                                                                                                                    1 CGGCGGCGUGAUGGCAUGCACUA 23
                                                                                                                                                              Best Local Similarity 73.9
Matches 17; Conservative
                                                                                                                                                         Query Match
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Human BACE G-cleaver ribozyme sequence #52.
                                                                         ADV04149 standard; RNA; 37
                                                                                                                                     (first entry)
                                                                                                                                     10-FEB-2005
                                                                                                       ADV04149;
                                               RESULT 9
                                                             ADV04149
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Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase; MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha; beta-secretase; BACE; human epidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; mepatitis B virus; HBV, hammerhead; HH; hairpin; NCH; inozyme; G-cleaver; amberzyme; UNAzyme; ONAzyme; naroer; breast cancer; Alzheimer's disease; disabetes; obesity; cardiac disease; heart disease; age-related disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human:

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990S-00406643
990S-0156236P.
990S-0156467P.
990S-00436430.
990S-0169100P.
                                                                                                                      2000WO-US023998
                                                                                                                               99US-0151713P.
                                                                                                   WO200116312-A2.
                                                                                          Homo sapiens.
                                                                                                                      30-AUG-2000;
                                                                                                                                             27-SEP-1999;
08-NOV-1999;
06-DEC-1999;
                                                                                                            08-MAR-2001.
                                                                                                                               31-AUG-1999;
                                                                                                                                    27-SEP-1999;
27-SEP-1999;
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Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-lb; PTB-1B; methionine aminopeptidase; MetAP-2; human telomerase; HTERT; protein kinase C alpha; PKC alpha; beta-secretase; BACE; human epidermal growth factor receptor-2; HERZ; c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; mepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inoxyme; G-cleaver; amberzyme; Zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease; diabetes; obesity; cardiac disease; heart disease; age-related disease;

Human BACE G-cleaver ribozyme sequence #30.

10-FEB-2005 (first entry)

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The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBRT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (HERZ/C-ert2/neu), phospholamban (PLN), presenilin-1 (ps-1), presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amborzyme, cinzyme, and/or DNAzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Alzheimer's disease, diseases, hepatitis B infections, and hepaticis and hepaticis and hepaticis and seases, hepatitis and hepaticis and hepaticis and seases, carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells and to detect the presence of specific RNA in a cell. The present invention. Note: Some SEQ ID Nos are repeated more than once in the sequence represents a ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the examples of the present sepecification, but these have different sequences associated with them.
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6e+02;
~hes 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 37 BP; 6 A; 12 C; 14 G; 0 T; 5 U; 0 Other;
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Local Similarity 73.9%; Pred, No. 6e+0:
les 17; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      Example 4; Page 365; 717pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
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Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase; hether?; human telomerase; hTERT; protein kinase C alpha; PKC alpha; beta secretase; BACB; human epidermal growth factor receptor-2; HERZ; c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inoxyme; G-cleaver; amberzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease; diabetes; obesity; cardiac disease; heart disease; age-related disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;

Human PLN G-cleaver ribozyme sequence #18.

(first entry)

10-FEB-2005

ADV17630;

ВЪ.

ADV17630 standard; RNA; 37

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Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.
hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
                                                                                                                                                                                                                                                                                                Usman N, Blatt L, Beigelman L, Burgin A;
Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 37 BP; 9 A; 7 C; 16 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Page 364; 717pp; English.
                                                                                                                        27-SEP-1999; 990S-0040643.
27-SEP-1999; 990S-0046643.
27-SEP-1999; 990S-0156467P.
08-NOV-1999; 990S-00436430.
06-DEC-1999; 990S-00474432.
29-DEC-1999; 990S-00474432.
29-DEC-1999; 990S-00476387.
30-DEC-1999; 990S-00776387.
20-MRR-2000; 2000US-00531025.
14-APR-2000; 2000US-00531025.
                                                                                                                                                                                                                                               23-MAY-2000; 2000US-00578223.
09-AUG-2000; 2000US-00636385.
                                                                                             30-AUG-2000; 2000WO-US023998
                                                                                                                                                                                                                                                                              (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                              Karpeisky A, Matulic-Adam.
Stinchcomb D, Beaudry A,
                                                                                                                                                                                                                                                                                                                                           WPI; 2001-244406/25.
                                                      WO200116312-A2.
                                                                                                                                                                                                                                                                                                   Mcswiggen J,
                                 Homo sapiens.
                                                                         08-MAR-2001
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The present invention trained by the strained controlled for their rule of also methods for their use to down regulate or inhibit the expression also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBR), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (HERZ/C-erb2/neu), phospholamban (PLN), prosenilin-1 (ps-1), presenilin-2 (ps-2), and hepatitis B wirus (HBN) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inoxyme), G-Cleaver, amberzyme, cinclude hammerhead (HH), hairpin, NCH (inoxyme), G-Cleaver, amberzyme, cinclude hammerhead (HH), hairpin, NCH (inoxyme), G-Cleaver, amberzyme, cinclude hammerhead (HH), hairpin, NCH (inoxyme), G-Cleaver, anderzyme, cinclude papatitis B infections, and hepatitis and hepatical as a calcinos, and hepatitis and hepaticis can also be used as diagnostic tools to examine genetic drift and mutations within diseased calcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased calcinoma. Note: Some SEQ ID Nos are repeated more than once in the invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.
present invention relates to the use of enzymatic nucleic acid
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Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.

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Chowrira

Burgin A;

Matulic-Adamic J, Sweedler D, Draper K, Ch Beaudry A, Zinnen S, Lugwig J, Sproat BS;

WPI; 2001-244406/25.

Stinchcomb D,

Mcswiggen J, Karpeisky A,

Beigelman L, Sweedler D, D

Blatt L,

99US-00436430. 99US-0169100P. 99US-00474432.

08-NOV-1999; 06-DEC-1999; 29-DEC-1999; 29-DEC-1999; 04-FEB-2000; 20-MAR-2000;

99US-0173612P 99US-00476387 2000US-00498824

30-AUG-2000; 2000WO-US023998

WO200116312-A2.

08-MAR-2001

Homo sapiens.

99US-0151713P 99US-00406643 99US-0156236P 99US-0156467P

31-AUG-1999 27-SEP-1999 27-SEP-1999 2000US-00531025 2000US-0197769P

14-APR-2000; 23-MAY-2000;

09-AUG-2000;

2000US-00636385

(RIBO-) RIBOZYME PHARM INC.

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The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBRT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (FBRZ/C-erbz/neu), phospholamban (PLN), presenilin-1 (ps-1), presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, cinclude hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, cinclude hammerhead (diseases e.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepatocellular carcinoma. The arzymatic nucleic acid molecules can also be used as diseased to account and metations within diseased
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1 CACGGGAGUGAUGGCAUGCACUA 23

RESULT 11

CAGCGGAGTGATGGCAAGCACGA 23

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69.2%;

17; Conservative

Local Similarity

Query Match Matches

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Claim 5; Page 87; 152pp; English
                                                                                                                                                                                                                                                                          Best Local Similarity
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                                                                                                                                                                                                                                                                                 Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase; MetAP-2; human tedomerase; hrERT; protein kinase C alpha; PKC alpha; beta-secretase; BACE; human epidermal growth factor receptor-2; HERZ; c-erb2; neu; phospholamban; PLN; presentlin-1; ps-1; presentlin-2; ps-2; amberiyme; zinzyme; DNAzyme; cancer; braitpin; NCH; inozyme; G-cleaver; amberzyme; zinzyme; and sease; beart disease; ade-related disease; diabetes; obesity; cardiac disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
cells and to detect the presence of specific RNA in a cell. The present sequence represents a ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.
                                                                                                 Gaps
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                                                                         Query Match 69.2%; Score 16.6; DB 5; Length 37; Best Local Similarity 73.9%; Pred. No. 6e+02; Matches 17; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Usman N, Blatt L, Beigelman L, Burgin A;
Matulic-Adamic J, Sweedler D, Draper K, Ch
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
                                                      Sequence 37 BP; 11 A; 8 C; 11 G; 0 T; 7 U; 0 Other;
                                                                                                                                                                                                                                                               Human BACE G-cleaver ribozyme sequence #31
                                                                                                                    1 CAGCGGAGTGATGGCAAGCACGA 23
                                                                                                                                         Example 4; Page 365; 717pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0156236P.
99US-0156236P.
99US-0156467P.
99US-00436430.
99US-0169100P.
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2000US-00498824.
2000US-00531025.
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                                                                                                                                                                                              ADV04128 standard; RNA; 37
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                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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08-NOV-1999;
06-DEC-1999;
29-DEC-1999;
29-DEC-1999;
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Karpeisky A,
                                                                                                                                                                                                                                          10-FEB-2005
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                                                                                                                                                                                                                     ADV04128;
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The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (MTBRT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (HERZ/C-erz2/meu), phospholamban (PLN), presenilin-1 (ps-1), presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HR), hairpin, NCH (inozyme), G-Cleaver, amberzyme, zinzyme, and/or DNAzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Alzheimer's disease, diseases, hepatitis B infections, and hepatitis and hepatitis B infections, and hepatitis and hepatitis and codecet the presence acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased calb and to detect the presence of specific RNA in a cell. The present sequence represents a ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 37 BP; 8 A; 10 C; 14 G; 0 T; 5 U; 0 Other;
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2; Mismatches
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The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition associated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid molecule, Hepatitis C virus, HCV; Hepatitis B virus, HBV; RNA stability; RNA expression; RNA synthesis, antisense; enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; amberzyme; G-cleaver ribozyme; decoy molecule; aptamer; HBV reverse transcriptase; Enhancer I region; viral replication; degenerative, disease state; HBV infection; HCV infection; cirrhosis; liver failure; hepatocellular carcinoma; hepatotropic; cytostatic; virucide; antiinflammatory; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                69.2%; Score 16.6; DB 6; Length 37; 73.9%; Pred. No. 6e+02; tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                Sequence 37 BP; 8 A; 7 C; 14 G; 0 T; 8 U; 0 Other;
                                                                                                                                                                                                                                                                                                            enzymatic nucleic acid molecule of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CAGCGGAGTGATGGCAAGCACGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CAGGGUAGUGAUGGCAUGCACUA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACD53318 standard; RNA; 37 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-2001; 2001US-00817879.
08-JUN-2001; 2001US-00877478.
08-JUN-2001; 2001US-0296876P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-2002; 2002WO-US009187.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HBV G-cleaver sequence #57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIBOZYME PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 73.9
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLATT L.
MACEJAK D.
MCSWIGGEN J.
MORRISSEY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEE P.
DRAPER K.
ROBERTS E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis B virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200281494-A1.
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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(MACE/)
(MCSW/)
(MORR/)
(PAVC/)
(LEEP/)
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(ROBE/)
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The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HHV) RNA. The nucleic acid molecules include antisense and enzymes, zinzymes, amberzymes, and G-cleaver ribozymes. DNAzymes, inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed are nucleic acid decoy molecules and aptamers that bind to HBV reverse transcriptase primer sequences, as well cranscriptase and/or HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV DNA. The nucleic acids may be used to modulate the expression of HBV compounds and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds and compounds and/or potential therapies directed against HBV, and compounds compounds and/or potential therapies directed against HBV, and compounds and compounds and/or potential therapies directed against HBV, and compounds compounds and/or potential therapies directed against HBV, and compounds and compounds and/or potential therapies directed against HBV, and compounds compounds and with a sequence of the HBV in the compounds and compounds and the present sequence represents one of the HBV riboxyme, carcinoma. The present sequence represents one of the HBV riboxyme, inozyme, discase, zinzyme, DNAzyme or amberzyme sequences disclosed in
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                                                                                             Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus
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ь,
П
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage; hepatitis B virus infection; hepatitis; hepatocellular carcinoma; cirrhosis; liver failure; lamivudine; interferon; genetic drift; virucide; hepatotropic; antiinflammatory; cytostatic.
    Lee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.2%; Score 16.6; DB 8; Length 37; 73.9%; Pred. No. 6e+02; ive 2; Mismatches 4; Indels
  Pavco P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis B virus (HBV) enzymatic nucleic acid #1471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 37 BP; 8 A; 10 C; 12 G; 0 T; 7 U; 0 Other;
  Mcswiggen J, Morrissey D,
                                                                                                                                                                              Example 1; Page 166; 387pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CAGCGGAGTGATGGCAAGCACGA 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-FEB-1994; 94US-00193627.
08-NOV-1999; 99US-00456430.
20-MAR-2000; 2000US-00531025.
24-OCT-2000; 2000US-0065385.
24-OCT-2000; 2000US-00695347.
08-JUN-2001; 2001US-00877478.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 73.9
nes 17; Conservative
    Macejak D,
Roberts E;
                                                              WPI; 2003-229207/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DRAP/) DRAPER K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2004054156-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-MAY-1992;
      Blatt L, N
Draper K,
                                                                                                                                             infection.
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10 CAGMTGMGTGMTGGCATACAGGAC 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 70.00
Best Local 17; Conservative
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/label= (
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                                                                                                                                                                                                                                                                                               The invention relates to an enzymatic nucleic acid molecule that specifically cleaves RNA derived from hepatitis B virus (HBV) and comprising one or more binding arms, without requiring the presence of a 2.0H group within the molecule for activity. The nucleic acids are useful for treating hepatitis B virus infection, hepatitis, hepatocellular carcinoma, cirrhosis and liver failure, either alone or in combination with other therapies such as lamivudine and interferons. The nucleic acids are useful as diagnostic tools to examine genetic drift and mutations within diseased cells, for detecting the presence of HBV RNA in a cell, for the study of RNA and for down-regulating gene expression of target genes in bacterial, fungal, viral, plant or mammalian cells. This sequence represents an enzymatic nucleic acid molecule which cleaves HBV RNA of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at
                                                                                                                                                                       Novel enzymatic nucleic acid molecule such as DNAzymes and inozymes specifically cleaving RNA derived from hepatitis B virus and comprising one or more binding arms, useful for treating hepatitis and cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, Y chromosome, DYS271, SNP; single nucleotide polymorphism; 88;
mutation detection, denaturing high performance liquid chromatography;
DHPLC; nitrogen containing composition; PCR; primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 37 BP; 8 A; 10 C; 12 G; 0 T; 7 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                          Morrissey D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6e+02;
                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 4013; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 6e+C
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CAGCCUAGUGAUGGCAUGCACUA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CAGCGGAGTGATGGCAAGCACGA 23
                                                                                      Mcswiggen JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         segdata.uspto.gov/seguence.html.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 73.9%;
es 17; Conservative
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(BLAT/) BLATT L.
(MCSW/) MCSWIGGEN J A.
(MORR/) MORRISSEY D.
                                                                                      Blatt L,
                                                                                                                                WPI; 2004-247781/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-743884/70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2003082557-A1.
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                                                                                        Draper K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Taylor PD;
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Matches
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The invention relates to preparing a double stranded DNA fragment for mutation detection by denaturing high performance liquid chromatography (DHELC) comprising including during the hybridisation, a nitrogen containing composition (of structure detailed in the specification). The double stranded DNA fragment corresponds to a wild type double stranded DNA fragment having a known nucleotide sequence. The method further comprises: (a) amplifying a section of the double stranded DNA fragment for mutation detection by PCR using a set of primers flanking the section, where at least one primer of the set incorporates a sequence comprising solely GC content on the S' end; (b) hybridising the amplification product of (a) with wild type double stranded DNA corresponding to the section, where a mixture comprising one or more including during the hybridisation, an amount of the nitrogen containing composition. The composition is included to increase the amount of the composition is included to increase the amount of the composition is included for mixture for mutation detection.
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denaturing high performance liquid chromatography, comprises including during hybridization composition comprising a nitrogen-containing organic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Also included are a product of the method above, a kit for preparing a double stranded DNA for mutation detection by liquid chromatography, a kit for hybridiaing a target nucleotide sequence with wild type DNA corresponding to the target sequence, and a kit for analysing a double stranded DNA for mutation detection by liquid chromatography. The method is useful for preparing a double stranded DNA fragment for mutation analysis, and for diagnosing a disease. The method improves the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 resolution between hereroduplex and homoduplex peaks even for mutations that are difficult to detect. The present sequence is a PCR primer used to amplify variants of the human Y chromosome locus DYS271 (which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contains 3 single nucleotide polymorphisms) and is used to demonstrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone cGMP-5 for allosteric modulation of hammerhead ribozyme by cGMP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      flavin mononucleotide; conformational change; molecular switch; CM; communication module; allosteric; sensing element; environmental; agricultural; clinical; industrial; genetic control; cGMP; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Communication module
/note= "Comprises substitution mutations"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= b
/note= "Cytosine substituted with Uracil"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 45 BP; 8 A; 11 C; 14 G; 7 T; 0 U; 5 Other;
                                                                                                                                                                                                                  Example 4; SEQ ID NO 4; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24
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Human NOGO G-Cleaver substrate sequence #29.

(first entry)

12-MAR-2002

ABK05366;

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constructed using harmmerhead ribozyme RNAs, comprising an actuator or catalytic domain, bridging domain and receptor or aptamer domain. The interaction of the receptor with a signalling agent like a ligand e.g., flavin mononuclectide (FMN) or physical signal, triggers a conformational change in the bridging domain, that modulates the catalytic or reporter activity of the actuactor domain. If functions as a molecular switch.

Communication module (CM) sequences can be inserted as the bridging domain, that enhances the allosteric properties. The ligand-specific sensors may be used as sensing elements in clinical, agricultural, clements for the regulation of gene expression. The present RNA sequence is the clone cGMP-5, isolated from G18' RNA population, after selective is the clone cGMP-5, isolated from G18' RNA population of mumbification of modulation of such the allosteric modulation of the mannerhead ribozymes by cGMPs. This clone comprises mutations in the aptamer domain (deletions) and communication module (substitutions)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel functional polynucleotides comprising an actuator domain, a receptor domain, and a bridging domain useful for generating highly specific polynucleotide sensors and as genetic control elements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The patent discloses multidomain polynucleotide molecular sensors,
                                                                                                                                                                                                                                                  *tag= h
note= "Guanine substituted with Cytosine"
                                                                                                                                                                                                      *tag= g
note= "Cytosine substituted with Adenine"
                                                                                                   label= Communication module
note= "Comprises substitution mutations"
                                                                                                                                                                 note = "Adenine substituted with Uracil"
                                                                                                                                                                                                                                                                                                    /*tag= i
/note= "Uracil substituted with Guanine"
"Uracil substituted with Guanine"
                                  d
"Corresponds to aptamer domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 32 BP; 7 A; 8 C; 11 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Fig 10A; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US025497
                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0106829P
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                                                                                     *tag= (
                                                                   29. .32
                   . .28
*tag=
                                                                                                                                                                                                   *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g,
                                                                                                                                                     *tag=
                                                     note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-365558/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Soukup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                       WO200026226-A1
                                                                                                                                                                                                                                                                                                                                                                                                                           29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAR-1999;
                    misc_feature
                                                                   misc_feature
                                                                                                                                      misc_feature
                                                                                                                                                                                     misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                        11-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Breaker RR,
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ö Gaps . 0 Length 32; 3; Indels Score 16.2; DB 3; Pred. No. 9.1e+02; 1; Mismatches 3; 22 AGCGGAGCGAUGGCAGCCACG 28 1,

67.5**%**; 81.0**%**;

Local Similarity 81.0 les 17; Conservative

datches

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Query Match

ABK05366 standard; RNA; 37

RESULT 18 ABK05366

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The invention relates to a nucleic acid molecule which down regulates capression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NGGO). The regulates expression of a neurite growth inhibitor gene (NGGO). The cucleic acids may be enzymatic nucleic acid cleaving an RNA molecule DNAxyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule consessing an NCH motif), a G-cleaver (cleaving RNA with a NNY motif) proposessing an NCH motif). The CD20-targetting nucleic acid is used to cleave RNA with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA cof CD20 in the presence of a divalent cation that is preferably MG^2+. Furthermore, it may be contacted with a cell to reduce CD20 activity of the classification in the comparise the use of one or more cof CD20. The treatment may further comptise the use of one or more cof creat lymphoma, leukaemia, He CD20 targetting nucleic acid with the level commune thrombocytopaenia, and inflammatory arthropathy. The NOGO-cleargetting nucleic acid may be cused to follicular NHL, lymphoma, immunocytoma (IMC), small B-cell lymphoma (MC), immunocytoma (IMC), small B-cell lymphoma, commune thrombocytopaenia, and inflammatory arthropathy. The NOGO-cleargetting nucleic acid may be contacted with a cell to reduce NOGO activity of the presence of a divalent having a condition associated with the level of coll and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more therefore the reatment may further comprise the use of one or more therefore the sused to the rapies. In particular, the NOGO-clargetting nucleic acid may be used to the condition associated with the level of the rapies. In particular, the NOGO-clargetting nucleic acid may be used to be accompanied.
                                                                                                                                                            Human; 88; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNAzyme; inozyme; deaver; amberzyme; intryme; locaver; amberzyme; intryme; locaver; amberzyme; intryme; locaver; amberzyme; lymphoma; leukaemia; human immunodeficiency virus; HIV associated NHL; lymphocytic leukaemia; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; demenia; inflammatory arthropath; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; Parkinson's disease; ataxia; Huntington's disease; substrate sequence; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chowrira BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 89; Page 92; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       central nervous system injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-FEB-2000; 2000US-0181797P.
28-FEB-2000; 2000US-0185516P.
06-MAR-2000; 2000US-0187128P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-FEB-2001; 2001WO-US004273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mcswiggen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLATT L.
MCSWIGGEN J.
CHOWRIRA B M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-607195/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200159103-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blatt L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BLAT/)
(MCSW/)
(CHOW/)
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3 GCGGAGTGATGGCAAGCACGA 23
                                                                                                                                                                                                                                                                                                                                                                                          23
                                                                                                                                                                                                                                                                                                                                                                                    3 GCCGAGUGAUGGCAUGCACUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK20721 standard; RNA; 37 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-MAY-2001; 2001WO-US015866.
                                                                                                                                                                                                                                                                                                                         67.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAY-2000; 2000US-00572021
                                                                                                                                                                                                                                                                                                                                   76.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Von Carlowitz I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RIBO-) RIBOZYME PHARM INC.
  obesity and heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-082995/11.
                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200188124-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jarvis T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amberzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK20721;
                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 20
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                                                                                                                                                                                                                                                                                                                                                       Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase; MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha; beta-secretase; BACE; human epidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inoxyme; G-cleaver; amberzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease; disbetes; obesity; cardiac disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; ss.
        (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (MLS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NGGO expression. The present sequence is a substrate sequence for a nucleic acid of the invention based on the human NGGO sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
 central nervous system (CNS) injury and cerebrovascular accident
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chowrira
                                                                                                                                                        ö
                                                                                                                              Score 16.2; DB 4; Length 37; Pred. No. 9.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beigelman L, Burgin A;
Sweedler D, Draper K, Ch
n S, Lugwig J, Sproat BS;
                                                                                                                                                      3; Indels
                                                                                                        Sequence 37 BP; 6 A; 8 C; 18 G; 0 T; 5 U; 0 Other;
                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beaudry A, Zinnen S,
                                                                                                                                                                                                                                                                                                                                  HBV G-cleaver ribozyme sequence #41.
                                                                                                                                                                            3 GCGGAGTGATGGCAAGCACGA 23
                                                                                                                                                                                          3 GGGGAGUGAUGGCAUGCACUA 23
                                                                                                                                                     3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Usman N, Blatt L,
Matulic-Adamic J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-AUG-1999; 99US-0151713P.
27-SEP-1999; 99US-016643.
27-SEP-1999; 99US-0166436P.
27-SEP-1999; 99US-0156470P.
08-NOV-1999; 99US-00436430.
29-DEC-1999; 99US-00476432.
29-DEC-1999; 99US-00476387.
04-FEB-2000; 2000US-00531025.
                                                                                                                                67.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                             ADV47946 standard; RNA; 37
                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                      16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-244406/25.
                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200116312-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stinchcomb D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mcswiggen J,
Karpeisky A,
                                                                                                                                                                                                                                                                                                            10-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAR-2001
                                                                                                                                                                                                                                                                                   ADV47946;
                                                                                                                                                      Matches
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The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (PTB-LB), methionine aminopeptidase (McLAP-2), human telomerase (HTBRT), protein kinase C alpha (PKC apha), beta-secretase (BACE), human epidermal growth factor receptor-2 (HERA/C-ert2/neu), phospholaban (PLM), presentlin-1 (ps-1), presentlin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucled nammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, zinzyme, and/or DNAzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Albraimer's disease, clabetes, obesity, cardiac disease e.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepatitis and seed as cardinoma. The enzymatic nucleic acid molecules can also be used as clasmostic tools to examine genetic drift and mutations within diseased cells and to detect the present cardinal present cardinal present cardinal presents are present cardinal presents and hepatitis and bepresents and present cardinal presents are presented and presents are presented and presents are presented and pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, hammerhead ribozyme, cytostatic, antitumour; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic; vulnerary; cancer; lymphoma; Ening's sarcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofibroma of tuberous sclerosis; port-wine stain; wound healing; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss; osterweber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mclaughlin F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 37 BP; 7 A; 8 C; 14 G; 0 T; 8 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ERG G-cleaver ribozyme, Seg ID No 3368.
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Example 6; Page 531; 717pp; English.
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The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for traating conditions selected from cancer. Lymphoma, Ewing's sarcoma, metanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, tumour angiogenesis, diabetic retinopathy, macular degeneration, cumour angiogenesis, diabetic retinopathy, macular degeneration, cumour angiogenesis, diabetic retinopathy, macular degeneration, sturge vulgaris, angiofibroma of tuberous sclerosis, port-whis stains, Sturge Weber syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. Leukaemia or tumour conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or chemotherapy treatment. (I) is useful for reducing ERG activity in a cell, by contacting (I) with RNM, in the presence of a divalent cation such as Mg2+. (I) is useful for diagnosis of conditions and diseases related to the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically cargeting genes that share homology with ERG gene or ERG fusion genes. ABK17354-ABK22719 represent nucleic acide, including antisense and centared positiones within regulate expression of ERG, and centared positiones of the invention cade, including antisense and centared modecules which regulate expression of ERG, and centared positiones.
Novel polynucleotide which down regulates expression of Ets-related gene, useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV; RNA stability; RNA expression; RNA synthesis; antisense; enzymatic nucleic acid; hammerhead ribozyme; bNAzyme; inozyme; zinzyme; amberzyme; G-cleaver ribozyme; decoy molecule; aptamer; HBV reverse transcriptase; Enhancer I region; viral replication; degemerative, disease state, HBV infection; HCV infection; cirrhosis; liver failure; hepatocellular carcinoma; hepatotropic; cytostatic; virucide; antiinflammatory; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.5%; Score 16.2; DB 6; Length 37; 76.2%; Pred. No. 9.2e+02; Live 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 37 BP; 7 A; 10 C; 12 G; 0 T; 8 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 GCGGAGTGATGGCAAGCACGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 GCGUAGUGAUGGCAUGCACUA 23
                                                                                                 Claim 5; Page 82; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACD53251 standard; RNA; 37 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002; 2002WO-US009187.
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08-JUN-2001; 2001US-00877478.
08-JUN-2001; 2001US-0296876P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HBV G-cleaver sequence #41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-SEP-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200281494-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACD53251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HEV) RNA. The nucleic acid molecules include antisense and enzymes, amberzymes, and shammerhead ribozymes. DNAzymes, inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed are nucleic acid decoy molecules and apteamers that bind to HBV reverse cranscriptase and/or HBV reverse transcriptase and/or HBV reverse transcriptase and/or they reverse transcriptase and/or they reverse transcriptase and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds char modulate the expression and/or replication of HCV. The compounds and methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocallular carrious are useful for methods of the present sequence represents one of the HBV ribozyme, incorpulation incyme, carcinoma. The present sequence represents one of the HBV ribozyme, incorpulation incyme, incorpulation and method of incyme, incorpulation and method incyme, incorpulation and methods of the incyme, incorpulation and methods of the incorpulation and methods of the present sequence represents one of the HBV ribozyme, incorpulation incyme, incorpulation and methods of the methods 
                                                                                                                                                                                                                                                                                                                                                                                                                         Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                        Lee
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                                                                                                                                                                                                                                                                                                        Pavco P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis B virus (HBV) enzymatic nucleic acid #1455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 37 BP; 7 A; 8 C; 14 G; 0 T; 8 U; 0 Other;
                                                                                                                                                                                                                                                                                                        Morrissey D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 165; 387pp; English.
                                                                                                                                                                                                                                                                                                             Mcswiggen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GCCGAGUGAUGGCAUGCACUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GCGGAGTGATGGCAAGCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADM61863 standard; RNA; 37 BP
24-OCT-2001; 2001US-0335059P.
05-DEC-2001; 2001US-0337055P.
                                                                    RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 76.2
nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the present invention
                                                                                                                                                                                                                                                                                                          Blatt L, Macejak D,
Draper K, Roberts E;
                                                                                                           MACEJAK D.
MCSWIGGEN J.
MORRISSEY D.
                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-229207/22
                                                                                                                                                                                                                                                            (ROBE/) ROBERTS E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis B virus
                                                                                                                                                                                                                LEE P.
DRAPER K.
                                                                                                                                                                                          PAVCO P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2004054156-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infection.
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                                                                                          (BLAT/) E
(MACE/) N
(MCSW/) N
(MORR/) N
(PAVC/) E
(LEEP/) I
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                                                                       (RIBO-)
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Matches
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The invention relates to antisense compounds, especially
oligonuclectides, which are targeted to a nucleic acid encoding inducible
conterior oxide synthase and which specifically hybridise to and modulate
compression of inducible nitric oxide synthase. The antisense compounds
control control antidiabetic, cardiovascular, cardiant,
control control antidiabetic, cardiovascular, cardiant,
control control antidiabetic, cardiovascular, cardiant,
control control antidiabetic activity. The antisense
coligonucleotides are useful for inhibiting the expression of inducible
coligonucleotides are useful for inhibiting the expression of inducible
coligonucleotides are useful for treating diseases or disorders associated
with inducible nitric oxide synthase, e.g. diabetes immunological
control cardiovascular disorder, neurological disorder or
control cardiovascular disorder. The antisense oligonucleotides are also
cuseful for research and diagnostics. The present sequence is that of an
antisense 2'-O-methoxyethyl gapmer oligonucleotide with a
cardiusense 2'-O-methoxyethyl gapmer oligonucleotide with a
control cardiovascular disorder oligonucleotide with a
cardiusense 2'-O-methoxyethyl gapmer oligonucleotide with a
cardiusen nucleotide 2'-MOE (2'-methoxyethyl) wings (cytidine
creaidues in the 2'-MOE wings are 5-methylcytidines) and targeted to human
control cardiovascular control cardiovascular control cardius and cardeted to human
control cardiovascular control cardiovascular control cardiovascular control cardiovascular cardiovascular control cardiovascular cardiovascular cardiovascular cardiovascular cardiovascular control cardiovascular cardiovascular cardiovascular control cardiovascular cardiovas
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                                                      /note= "phosphorothioate backbone, 5' and 3' four nucleotide 2'-MOE (2'-O-methoxyethyl) wings (the cytidine residues in the 2'-MOE wings are 5-methylcytidines) and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense oligonucleotides for modulating the expression of inducible nitric oxide synthase in cells or tissues, particularly useful for treating e.g. immunological, cardiovascular or neurological disorders, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase; MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha; beta-secretase; BACB; human epidermal growth factor receptor-2; HERZ; c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18 BP; 4 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 15; Page 83; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cowsert LM;
'*tag= a
'mod base= OTHER
                                                                                                                                                                                                                                                                                                                     15-JAN-2001; 2001WO-US001381.
                                                                                                                                                                                                                                                                                                                                                                           24-JAN-2000; 2000US-00490208.
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                                                                                                                                                deoxy gap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 TGATGGCAAGCACGAC
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ses 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bennett CF, Dean NM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-465340/50.
                                                                                                                                                                                                         WO200152902-A1
                                                                                                                                                                                                                                                               26-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ischemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an enzymatic nucleic acid molecule that specifically clasves RNA derived from hepatitis B virus (HBV) and comprising one or more binding arms, without requiring the presence of a 2.0H group within the molecule for activity. The nucleic acids are useful for treating hepatitis B virus infection, hepatitis, hepaticis, hepatocilular carcinoma, cirrhosis and liver failure, either alone or in combination with other therapies such as lamivudine and interferons. The nucleic acids are useful as diagnostic tools to examine genetic drift and mutations within diseased cells, for detecting the presence of HBV RNA in a cell, for the study of RNA and for down-regulating gene expression of target genes in bacterial, fungal, viral, plant or mammalian cells. This sequence represents an enzymatic nucleic acid molecule which cleaves HBV RNA of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel enzymatic nucleic acid molecule such as DNAzymes and inozymes specifically cleaving RNA derived from hepatitis B virus and comprising one or more binding arms, useful for treating hepatitis and cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense oligonucleotide; inducible nitric oxide synthase; NOS; modulate expression; immunomodulator; antidiabetic; cardiovascular; cardiant; neuroprotective; vasotropic; ischaemia; reperfusion injury; 2'-0-methoxyethyl; phosphorothioate; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gapв
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 37 BP; 7 A; 8 C; 14 G; 0 T; 8 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mcswiggen JA, Morrissey D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 3997; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                               92US-008B2712.
94US-00193627.
99US-00436430.
2000US-00531025.
2000US-00636385.
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                                                         15-JAN-2003; 2003US-00342902
                                                                                                                                                                                                                                                            24-OCT-2000; 2000US-00696347
08-JUN-2001; 2001US-00877478
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                                                                                                                                                                                                                                                                                                                                                                                                      MCSWIGGEN J A.
MORRISSEY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blatt L,
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                                                                                                                                                                                                                                                                                                                                                   DRAPER K.
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modified base
                                                                                                               14-MAY-1992;
07-FEB-1994;
08-NOV-1999;
                                                                                                                                                                                                   20-MAR-2000;
09-AUG-2000;
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(MCSW/)
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hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver; amborzyme; and isease; and sease; and sease; disease; disease; beatt disease; agg-related disease; heart disease; agg-related disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
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99US-0156236P.
99US-0156467P.
99US-010436430.
99US-0164432.
99US-0173612P.
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                                                                                                                                                                                                         (RIBO-) RIBOZYME PHARM INC
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                                                        WO200116312-A2.
                                           Homo sapiens.
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                                                                                                                                   06-DEC-1999;
29-DEC-1999;
29-DEC-1999;
30-DEC-1999;
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Blatt L, Beigelman L, Burgin A; damic J, Sweedler D, Draper K, Ch A, Zinnen S, Lugwig J, Sproat BS; Matulic-Adamic J, Sweed Beaudry A, Zinnen S, Stinchcomb D,

WPI; 2001-244406/25.

Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.

Example 3; Page 266; 717pp; English.

The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBRT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (IRER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1), presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-claever, ambozryme, include hammerhead (HH), hairpin, NCH (inozyme), G-claever, ambozryme, cinclude hammerhead (HH), hairpin, NCH (inozyme), G-claever, ambozryme, and or transmerting cancer, in particular breast cancer, Alzheimer's disease, diseases, bepatitis B infections, and hepatitis and hepaticis and hepatitis and calcineus within diseased calcinear carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased calcinear represents an anti human ribozyme used in the examples of the present invention, but these have different sequences associated with

Seguence 36 BP; 8 A; 6 C; 13 G; 0 T; 9 U; 0 Other;

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Query Match 65.8%; Score 15.8; DB 5; Length 36; Best Local Similarity 78.9%; Pred. No. 1.4e+03; Matches 15; Conservative 2; Mismatches 2; Indels
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2 GGAGUGAUGGCAUGCACUA 20

BP

ADU94721 standard; RNA; 36

RESULT 25 ADU9472 (first entry)

10-FEB-2005

ADU94721;

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Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase; hetaPa-2, human tedomerase, hTERT; protein kinase C alpha; PKC alpha; beta-secretae; BACE; human epidermal growth factor receptor-2; HBR2; c-erb2; neu; phospholamban; PLN; preseniln-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver; amberzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease; diabetes; obesity; cardiac disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
                                       Human TERT G-cleaver ribozyme sequence #143.
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99US-00406643.
99US-0156236P.
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                                                                                                                                                                           Homo sapiens.
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04-FEB-2000;
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29-DEC-1999;
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Burgin A; Chowrira Beigelman L, Burgin A; Sweedler D, Draper K, Ch n S, Lugwig J, Sproat BS; Usman N, Blatt L, Beig Matulic-Adamic J, Swee Beaudry A, Zinnen S, Blatt L, Mcswiggen J, Ur Karpeisky A, Ma Stinchcomb D, I

WPI; 2001-244406/25.

Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.

Example 1; Page 303; 717pp; English.

The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTERT), protein kinase C alpha) (PRC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (HERZ/c-erb2/neu), phospholamban (PLM), presentiln-1 (ps-1), presentiln-2 (ps-2), and hepstitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), d-cleaver, amberzyme, zinzyme, and/or DNAzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Alzheimer's disease,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enzymatic nucleic acid molecule; gene expression; down regulation, protein-tyrosine-phosphatase-lb; PTB-1B; methionine aminopeptidase; MetAP-2; human telomerase; hTERT; protein kinase Calpha; PKC alpha; beta-secretase; BACE; human epidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver; amberzyme; zinzyme; DNAzyme; cancer; beast cancer; Alzheimer's disease; disbetes; obesity; cardiac disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
diabetes, obesity, cardiac diseases e.g. heart disease, age-related diseases, heparitis B infections, and hepatitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells and to detect the presence of specific RNA in a cell. The present sequence represents a ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.
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Beaudry A, Zinnen S, Lugwig J, Sproat BS;
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                                                                                                                                                                                                     Sequence 36 BP; 8 A; 9 C; 13 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beigelman L,
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14-APR-2000; 2000US-0197769P.
23-MAY-2000; 2000US-00578223.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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29-DEC-1999;
30-DEC-1999;
04-FEB-2000;
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08-NOV-1999;
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27-SEP-1999
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The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBRT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (HER2/c-erb2/neu), phospholamban (PLM), presentlin-1 (ps-1), presentlin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (incayme), G-cleaver, amberzyme, zinzyme, and/or DNAzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Albrahemer's disease, diseases, hepatitis B infections, and hepatitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as disponsitic tools to examine genetic drift and mutations within diseased cells and to detect the presente expression of the present sections are presented and mutations within diseased cells and to detect the presence of specific RNA in a cell. The present sections are presented and presen
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are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.
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Pred. No. 1.4e+03;
2; Mismatches 2; Indels
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                                                                                                                                            Example 1; Page 307; 717pp; English
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nes 15; Conservative
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08-NOV-1999;
06-DEC-1999;
29-DEC-1999;
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27-SEP-1999
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The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBR), protein kinase C alpha (PKC alpha), beta-secretase (BACB), human epidermal growth factor receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1), presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), haripin, NCH (inozyme), G-cleaver, amberzyme, include hammerhead (HH), paripin, NCH (inozyme), G-cleaver, amberzyme, include hammerhead (HH), paripin, NCH (inozyme), G-cleaver, amberzyme, include hammerhead (Greases e.g. heart disease, age-related diseases, diseases, age-related diseases, hepatitis B infections, and hepatitis and hepaticis and hepatitis and hepa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                             Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A;
Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira
Stinchcomb D, Beaudry A, Zinnen S, Lugwig J, Sproat BS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 36 BP; 6 A; 9 C; 15 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 299; 717pp; English.
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                                                          04-FEB-2000; 2000US-00498824.
20-MAR-2000; 2000US-00531025.
14-APR-2000; 2000US-0197769P.
23-MAY-2000; 2000US-00578223.
09-AUG-2000; 2000US-00636385.
99US-0173612P.
                                                                                                                                                                                                                                                   (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       obesity and heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-244406/25.
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                                   30-DEC-1999;
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Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.

WPI; 2001-244406/25.

Karpeisky A, N Stinchcomb D,

Mcswiggen J,

Example 2; Page 211; 717pp; English.

Usman N, Blatt L, Beigelman L, Burgin A; Matulic-Adamic J, Sweedler D, Draper K, Chowrira B; Beaudry A, Zinnen S, Lugwig J, Sproat BS;

99US-0151713P. 99US-00406643. 99US-0156236P. 99US-0156467P.

27-SEP-1999; 27-SEP-1999; 27-SEP-1999; 08-NOV-1999;

30-AUG-2000; 2000WO-US023998

WO200116312-A2

08-MAR-2001

Homo sapiens.

99US-00474432 99US-0173612P

29-DEC-1999; 29-DEC-1999; 30-DEC-1999;

04-FEB-2000; 20-MAR-2000;

99US-00476387 2000US-00498824

99US-00436430 99US-0169100P 2000US-00531025 2000US-0197769P

2000US-00578223 2000US-00636385

09-AUG-2000; 14-APR-2000; 23-MAY-2000;

(RIBO-) RIBOZYME PHARM INC.

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Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-lb; PTB-1B; methionine aminopeptidase; hetherAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha; beta-secretase; BACE; human expidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver; amberzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease; disease; age-related disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human PTP-1B G-cleaver ribozyme sequence #110.
2 GGAGUGAUGGCAUGCACUA 20
                                                                                                                                                                                                                                                                ADM90363 standard; RNA; 36 BP.
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RESULT 29 ADU85545

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The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (MTBRT), protein Kinase C alpha (PKC alpha), beta-secretase (BACB), human epidermal growth factor receptor-2 (pse-2b2/neu), phospholamban (PLN), presentlin-1 (ps-1), presentlin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-claaver, amberzyme, cinclude hammerhead (HH), hairpin, NCH (inozyme), G-claaver, amberzyme, cinclude hammerhead (HH), hairpin, NCH (inozyme), G-claaver, amberzyme, cinclude hammerhead (HH), hairpin, NCH (inozyme), G-claaver, amberzyme, cardiac diseases e.g. heart disease, apserbliar carcinoma. The methods of the invention are useful fashes, obesity, cardiac diseases e.g. heart disease, and hepatitis and hepatitis and hepatitis and hepatitis and hepatitis and calcader acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased calcader capresents a ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 36 BP; 8 A; 5 C; 15 G; 0 T; 8 U; 0 Other;
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Best Local Similarity
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RESULT 30
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                                                                                                                                                                       Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-lb; PTB-1B; methionine aminopeptidase; MetAP-2; human telomerase; hTERT; protein kinase Calpha; PKC alpha; beta-secretase; BACE; human epidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; PLN; presentlin-1; ps-1; presentlin-2; ps-2; mepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inoxyme; G-cleaver; amberzyme; zinzyme; DNAzyme; cancer; branchimer's disease; disease; aderetes; obesity; cardiac disease; heart disease; age-related disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.
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Chowrira
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Matulic-Adamic J, Sweedler D, Draper K, Ch
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
                                                                                                                                  Human MetAP-2 G-cleaver ribozyme substrate seguence #133.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 264; 717pp; English.
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27-SEP-1999; 99US-00406643.
27-SEP-1999; 99US-0156267P.
08-NOV-1999; 99US-0156467P.
06-DEC-1999; 99US-0169100P.
29-DEC-1999; 99US-0173612P.
30-DEC-1999; 99US-0173612P.
30-DEC-1999; 99US-0173612P.
30-DEC-1999; 99US-0173612P.
30-DEC-1999; 99US-0173612P.
30-DEC-1999; 99US-0173612P.
30-DEC-1999; 99US-0173612P.
31-APR-2000; 2000US-0197769P.
  BP.
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ADU85545 standard; RNA; 36
                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-244406/25.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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Karpeisky A,
                                                                                         10-FEB-2005
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                                           ADU85545;
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sequence represents a substrate/target sequence for a ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.
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                                                                                                                                                                              Length 36;
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Matulic-Adamic J, Sweedler D, Draper K, Ch
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
                                                                                                                                                                                                                               2; Indels
                                                                                                                             Sequence 36 BP; 8 A; 6 C; 13 G; 0 T; 9 U; 0 Other;
                                                                                                                                                                           Score 15.8; DB 5;
Pred. No. 1.4e+03;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human PTP-1B G-cleaver ribozyme sequence #108.
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                                                                                                                                                                                                                            2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADM90361 standard; RNA; 36 BP.
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99US-00436430.
99US-0169100P.
99US-00474432.
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78.9%;
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2000US-00578223
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99US-0156236P
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99US-00476387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-FEB-2005 (first entry)
                                                                                                                                                                                                        Best Local Similarity 78.9
Matches 15; Conservative
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08-NOV-1999;
06-DEC-1999;
29-DEC-1999;
30-DEC-1999;
04-FEB-2000;
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Karpeisky A,
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23-MAY-2000;
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27-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADM90361;
                                                                                                                                                                              Query Match
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The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBRT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (HERZ/c-erbZ/neu), phospholamban (PLN), presenilin-1 (ps-1), presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, zinzyme, and/or DNAzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Alzheimer's disease, diabetes, obesity, cardiac diseases e.g. heart disease, age-related diseases, beptitis B infections, and hepaticis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased calls and to detect the presence of specific RNA in a cell. The present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-lb; PTB-1B; methionine aminopeptidase; metha-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha; beta-secretase; BACE; human epidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; DKI; presenilin-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; halrpin; NCH; inozyme; G-cleaver; amberzyme; zinzyme; DMAzyme; cancer; breast cancer; Alzheimer's disease; disease; disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 36 BP; 10 A; 6 C; 14 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human TERT G-cleaver ribozyme sequence #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 GGAGTGATGGCAAGCACGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GGAGUGAUGGCAUGCACUA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0151713P.
99US-00406643.
99US-0156236P.
99US-0156467P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADU94468 standard; RNA; 36 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-AUG-2000; 2000WO-US023998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 78.9
nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200116312-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-FEB-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADU94468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches
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990S-0169100P. 990S-00474432. 990S-0173612P. 99US-00476387. 2000US-00498824.

29-DEC-1999; 29-DEC-1999;

06-DEC-1999;

27-SEP-1999; 27-SEP-1999; 08-NOV-1999;

27-SEP-1999

30-DEC-1999; 99US-00476387. 04-FEB-2000; 2000US-00498824. 20-MAR-2000; 2000US-00531025.

2; Indels

2; Mismatches

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The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBAT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (IERZ/O-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1), presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, cinclude hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, cinclude hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, cinclude hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, cardiac diseases e.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepaticis and hepatitis and hepaticis and hepatitis and carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased calls and to detect the presence of specific RNA in a cell. The present sequence represents a ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.
                                                                                                                                                                                                                         Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;
                                                                                                                                  Chowrira
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15.8; DB 5; Length 36;
Pred. No. 1.4e+03;
2; Mismatches 2; Indels
                                                                                                                                Agrulic-Adamic J, Sweedler D, Draper K, Ch
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
                                                                                                              Burgin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 36 BP; 6 A; 9 C; 15 G; 0 T; 6 U; 0 Other;
                                                                                                                  Beigelman L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Chkl ribozyme SEQ ID NO: 2138.
                                                                                                                                                                                                                                                                                                          Example 1; Page 299; 717pp; English.
                                                                                                                Blatt L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GGAGUGAUGGCAUGCACUA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 GGAGTGATGGCAAGCACGA 23
                                                                                                                                    Matulic-Adamic J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH96713 standard; RNA; 37 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-FEB-2001; 2001WO-US003504
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14-APR-2000; 2000US-0197769P.
23-MAY-2000; 2000US-00578223.
09-AUG-2000; 2000US-00636385.
                                                                            (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNA cleavage; cancer; ss.
                                                                                                                                                                                           WPI; 2001-244406/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                  Mcswiggen J, Ut
Karpeisky A, Mi
Stinchcomb D, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157206-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (MOGO). The regulates expression of a neurite growth inhibitor gene (MOGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNAzyme) an Inozyme (an endolytic nucleic acids (e.g. a ribozyme or a DNAzyme) an Inozyme (an endolytic nucleic acid cleaving RNA with a NGM with an NGN with an NGN molecule of CD20 in the presence of a divalent cation that is preferably MG<sup>2</sup> +. Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more of CD20. The treatment may further comprise the use of one or more treat lymphoma, leukaemia, B-cell lymphoma, low-grade or folicular NHI. Jymphoma, leukaemia, HIV (human immunodeficiency virus) associated WHI. Mantle-cell lymphoma (MCI), immunocytoma (IMC) small B-cell lymphocytic lymphoma (MCI), immunocytoma (IMC), small B-cell lymphocytic lymphoma (MCI), immunocytoma (IMC) small B-cell lymphocytic lymphoma (MCI), immunocytoma (IMC), small B-cell lymphocy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; notropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOG0; hammerhead ribozyme; DNAzyme; inozyme; d-cleaver; amberzyme; inizyme; j-cleaver; amberzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HTV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
                                                                                 Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructe, which down regulate expression of a CD20 gene or neuxite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.8%; Score 15.8; DB 4; Length 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.4e+03;
2; Mismatches 2,
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                                                                                                                                                                                                                              Claim 89; Page 93; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 GGAGTGATGGCAAGCACGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAGUGAUGGCAUGCACUA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK08475 standard; RNA; 37 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Conservative
                           WPI; 2001-607195/69.
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ABK08475
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                                                                                                                                                                                                                                                                                                                                                                        The present invention provides nucleic acid molecules capable of downregulating the expression of the human checkpoint kinase-1 (Chkl) gene. These may be antisense or ribozyme sequences, and are useful in the treatment of diseases associated with conditions affected by Chkl levels, including cancer. The present sequence is an oligonucleotide described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOG0; hammerhead ribozyme; DNAzyme; inozyme; G-Cleaver; amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCI; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy:induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease; substrate sequence; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
                                                                                                                                                                                                Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid molecules, which downregulates expression of a checkpoint kinase-1 gene, useful for treating colorectal, lung, breast or prostate cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                       Mcswiggen J, Booher RN, Holman PS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.8%; Score 15.8; DB 4; Length 37; 78.9%; Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 37 BP; 9 A; 7 C; 11 G; 0 T; 10 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
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                                                                                                                                                                                                                                                                                                                     Claim 5; Page 67; 115pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 GGAGUGAUGCAUGCACUA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 GGAGTGATGGCAAGCACGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-FEB-2001; 2001WO-US004273.
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28-FEB-2000; 2000US-0185516P.
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(RIBO-) RIBOZYME PHARM INC.
(FATT/) FATTAEY A R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK05427 standard; RNA; 37
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Best Local Similarity 78.9'
Matches 15; Conservative
                                                                                    Jarvis T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mcswiggen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHOWRIRA B M.
                                                                                                                                             WPI; 2001-496922/54.
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MCSWIGGEN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200159103-A2.
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                                                                                    Fattaey AR,
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RESULT 33 ABK05427

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Blatt L,

MCSW/) CHOM/) BLAT/)

Homo

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(BLAT/) (MCSW/)
        (RIBO-)
          (CHOM/)
  S C
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The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down crepulates expression of a neurite growth inhibitor gene (NGGO). The cregulates expression of a neurite growth inhibitor gene (NGGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a nucleic acids may be enzymatic nucleic acid cleaving an RNA moltip presence of a divalent cation that is preferably MG 2+.

CC DNAZYME (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA with a YGY moutif). The CD20-targetting nucleic acid is used to cleave RNA cf CC CD in the presence of a divalent cation that is preferably MG 2+.

CC FCD20. The treatment may further compition associated with the level cf CD20. The treatment may further compities the use of one or more creat lymphoma, leukaemia, B-c21 lymphoma, low-grade or follicular non-therapies. In particular, he CD20 targetting nucleic acid may be used to treat lymphoma (MCL), immunocytoma (MNC), small B-c21 lymphocytic lymphocytic lymphoma, immunocytoma (MCL), small B-c21 lymphocytic lymphocytic lymphocytopaenia, and inflammatory arthropathy. The MCGO activity of the crasence of a divalent cation that a preferably MG 2+. Purthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the contacted with a cell to reduce MCGO activity of the nucleic acid may farther compathy, and celebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, and/or oth chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease; substrate sequence; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease. Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NOGO expression. The presensequence is a substrate sequence for a nucleic acid of the invention based on the human CD20 sequence Chowrira BM; Claim 31; Page 152; 200pp; English. central nervous system injury. 11-FEB-2000; 2000US-0181797P. 28-FEB-2000; 2000US-0185516P. 06-MAR-2000; 2000US-0187128P. 09-FEB-2001; 2001WO-US004273 RIBOZYME PHARM INC. BLATT L. Mcswiggen J, MCSWIGGEN J. CHOWRIRA B M. WPI; 2001-607195/69. 40200159103-A2. 16-AUG-2001 Synthetic. Blatt L,

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Sequence 37 BP; 6 A; 8 C; 12 G; 0 T; 11 U; 0 Other;
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; 0 Length 37; 2; Indels 65.8%; Score 15.8; DB 4; 78.9%; Pred. No. 1.4e+03; 2; Mismatches 15; Conservative Best Local Similarity Matches 15; Conservat Query Match

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Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic; antinflammatory; chronic obstructive pulmonary disease; COPD; asthma; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
                                                                                                                                                                                                                                                                                                                                                                                            Ensymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.
                                                                                                                                                                                                                                                                                                                                            Szymkowski DE;
                                                                                                                                                                                                                                                                                                                                             Mcswiggen J, Mckenzie T, Ayers D,
                                                                                                                   Human CLCA1 gene enzymatic nucleic acid #3492.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 86; 152pp; English.
ABK59121 standard; RNA; 37 BP
                                                                                                                                                                                                                                                                09-AUG-2001; 2001WO-US024970.
                                                                                                                                                                                                                                                                                   09-AUG-2000; 2000US-0224383P.
                                                                                                                                                                                                                                                                                                     (RIBO-) RIBOZYME PHARM INC.
(SYNT ) SYNTEX USA LLC.
(THOM/) THOMPSON J.
                                                                                                   (first entry)
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                                                                                                                                                                                   acetylcysteine.
                                                                                                                                                                                                                          WO200211674-A2.
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                                                                                                                                                                                                                                                                                                                                               Thompson J,
                                                                                                   02-JUL-2002
                                                                               ABK59121;
            'n
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                                                   ABK5912
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The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic libroals, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition associated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, archibererials, vaccinations, acetylcysterine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of cLCA1 in a cell. This sequence represents an ö Gaps ö 65.8%; Score 15.8; DB 6; Length 37; 78.9%; Pred. No. 1.4e+03; ive 2; Mismatches 2; Indels Sequence 37 BP; 8 A; 6 C; 16 G; 0 T; 7 U; 0 Other; enzymatic nucleic acid molecule of the invention 5 GGAGTGATGCCAAGCACGA 23 Best Local Similarity 78.9 Matches 15; Conservative Query Match В ò

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Human; chloride channel calcium activated 1; CLCA1; 88; antia8thmatic; antiinflammatory; chronic obstructive pulmonary disease; OOPD; asthma; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thompson J, Mcswiggen J, Mckenzie T, Ayers D,
                                                                                             Human CLCA1 gene enzymatic nucleic acid #3526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 87; 152pp; English.
ABK59155 standard; RNA; 37 BP
                                                                                                                                                                                                                                                                                                                            09-AUG-2001; 2001WO-US024970.
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                                                             02-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                            (SYNT ) SYNTEX USA LLC. (THOM/) THOMPSON J.
                                                                                                                                                                                                                                                                                                                                                                                           (RIBO-) RIBOZYME PHARM
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                                                                                                                                                                                              acetylcysteine
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                                                                                                                                                                                                                               Homo sapiens.
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                                ABK59155;
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The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition associated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an
                                                                                                                                                                          Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic; antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mcswiggen J, Mckenzie T, Ayers D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enzymatic nucleic acid molecule of the invention
                                                                                                                                             Human CLCA1 gene enzymatic nucleic acid #3549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Page 88; 152pp; English.
                                             ABK59178 standard; RNA; 37 BP.
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                                                                                                              02-JUL-2002 (first entry)
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Best Local Similarity 78.37
Best Local Si Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-217145/27.
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                                                                                                                                                                                                                                                                                                         WO200211674-A2.
                                                                                                                                                                                                                                              acetylcysteine
                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thompson J,
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                                                                                ABK59178;
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Szymkowski DE;

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The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition case useful for treatment of CLCA1 activity in a cell, hence, are useful for treatment of a condition a condition to more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibacterials, vaccinations, acetyloysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an
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Pred. No. 1.4e+03;
}; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 37 BP; 8 A; 5 C; 14 G; 0 T; 10 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enzymatic nucleic acid molecule of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK05394 standard; RNA; 37 BP.
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Matches 15; Conser
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Gaps

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2; Indels

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GGAGUGAUGGCAUGCACUA 23 S GGAGTGATGGCAAGCACGA 23

8 g RESULT 37 ABK59155

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12-MAR-2002 (first entry)
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Human NOGO G-Cleaver substrate seguence #57.

cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOG0; hammerhead ribozyme; DNAzyme; lnozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin; e lymphoma; MHL; lymphocytic leukaemia; human immunodeficiency virus; HV associated NHL; mantle-cell lymphoma; MCI; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy·induced neuropathy; ampotrophic lateral sclerosis; Parkinson's disease; ataxia; Huntington's disease; substrate sequence; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease. Human; 88; antisense therapy; cytostatic; antiinflammatory; haemostatic;

sapiens. Synthetic. QWQF

WO200159103-A2.

16-AUG-2001

09-FEB-2001; 2001WO-US004273

11-FEB-2000; 2000US-0181797P. 28-FEB-2000; 2000US-0185516P. 06-MAR-2000; 2000US-0187128P.

(RIBO-) RIBOZYME PHARM INC. (BLAT/) BLATT L. (MCSW/) MCSWIGGEN J. (CHOW/) CHOWRIRA B M.

Chowrira BM; Mcswiggen J, Blatt L,

WPI; 2001-607195/69.

Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury.

Claim 89; Page 92; 200pp; English.

The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neutite growth inhibitor gene (NGGO). The regulates expression of a neutite growth inhibitor gene (NGGO). The nucleic acids may be enzymatic nucleic acid cleaving an RNA molecule DNAzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NNN motif), a zinzyme (cleaving RNA with an NNN motif), a zinzyme (cleaving RNA with a YOY motif). The CD20-targetting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg^2+. Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more chargeting incleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-Hodgkin's lymphoma inmunodeficiency virus) associated NHL, lymphoma, leukaemia, HIV (human immunodeficiency virus) associated NHL, lymphoma, clenkaemia, HIV (human immunodeficiency virus) associated NHL, lymphoma, clenkaemia, HIV (human immunodeficiency virus) associated NHL, lymphoma, clenkaemia, and inflammatory arthropathy. The NOGO gene in the presence of a divalent cation that is preferably Mg^2+. Furthermore, the cucleic acid may be contacted with a cell to reduce NOGO activity of the nucleic acid may be contacted with a cell to reduce NOGO activity of the cucleic acid may be the NOGO-targetting nucleic acid may be used to treat a patient having a condition associated with the level of NOGO-trargetting nucleic acid may be contacted with a cell to reduce NOGO activity of the cucleic acid may be the NOGO-targetting nucleic acid may be contacted with a cell to reduce NOGO activity of the nucleic acid may be the NOGO-targetting nucleic acid may be one or more corrected with NOGO-targetting nucleic acid may be

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NGGO expression. The present sequence is a substrate sequence for a nucleic acid of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO). The
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                                                                                                                                                                 65.0%; Score 15.6; DB 4; Length 37; 72.7%; Pred. No. 1.8e+03;
                                                                                                                                                                                                    4; Indels
                                                                                                                             Sequence 37 BP; 8 A; 9 C; 12 G; 0 T; 8 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human NOGO G-Cleaver substrate sequence #64.
                                                                                                                                                                                                    Mismatches
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                                                                          sequence is a substrate sequence
based on the human NOGO sequence
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06-MAR-2000; 2000US-0187128P.
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                                                                                                                                                                                                                                                                                                                                                                    ABK05401 standard; RNA; 37
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nes 16; Conservative
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MCSWIGGEN J.
CHOWRIRA B M.
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Synthetic.
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(MCSW/) N
(CHOW/)
                                                                                                                                                                   Query Match
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CC DNAZYME) an Inozyme (an endolytic nucleic acids (e.g. a ribozyme or a DNAZYME) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NCH wotif), a cainzyme (cleaving RNA with an NCH motif) properties of a divalent of a zinzyme (cleaving RNA with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA of CC of CD20 in the presence of a divalent cation that is preferably Mg^2+.

CC of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targetting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic creat lymphoma (MLL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immunodeficiency virus) associated NHL, lymphocytic lymphoma, immunodeficiency virus) associated NHL, immune-cell immunocytoma (IMC), small B-cell lymphocytic lymphoma, immunodeficiency virus) associated NHL, lymphocytic lymphoma, immunodeficiency with a cell to reduce NGGO activity of the creatment may further comprise the use of one or more coll and treat a patient having a condition associated with the level of NGGO, horeign virus associated with the level of therapies. In particular, the NGGO-cleargetting nucleic acid may be contacted with a cell to reduce NGGO activity of the creatment may further comprise the use of one or more coll and treatment may further comprise the use of one or more coll and treatment may further comprise the use of one or more coll and treatment may further neurogenese coll and treatment may further c
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Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and

Claim 89; Page 92; 200pp; English.

central nervous system injury.

Chowrira BM;

Blatt L, Mcswiggen J, CHOWRIRA B M.

WPI; 2001-607195/69.

11-FEB-2000, 2000US-0181797P. 28-FEB-2000, 2000US-0185516P. 06-MAR-2000, 2000US-0187128P.

RIBOZYME PHARM INC

MCSWIGGEN J.

(CHOM/) (MCSM/)

BLATT L.

(RIBO-) (BLAT/)

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Gaps
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0
65.0%; Score 15.6; DB 4; Length 37; 72.7%; Pred. No. 1.8e+03;
                              4; Indels
                                 2; Mismatches
                                                                  2 AGCGGAGTGATGGCAAGCACGA 23
                                                                                    2 AGAGAAGUGAUGGCAUGCACUA 23
               Best Local Similarity 72.7
Matches 16; Conservative
     Query Match
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Human; 88; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNAzyme; inOzyme; G-Cleaver; amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCI; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; Parkinson's disease; ataxia; Huntington's disease; substrate sequence; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human NOGO G-Cleaver substrate sequence #48.
                                                                                                                               ABK05385 standard; RNA; 37 BP.
                                                                                                                                                                                                                                                                                                                                                                            12-MAR-2002 (first entry)
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                                                                                                                                                                                                                                                         ABK05385;
RESULT 40
                                                               ABKO5385
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The invention relates to a nucleic acid molecule which down regulates expression of a cD20 gene and a nucleic acid molecule which down control of a cD20 gene and a nucleic acid molecule which down cregulates expression of a neurite growth inhibitor gene (NOGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a nucleic acids may be enzymatic nucleic acid cleaving RNA with a NVB moitl), a G-cleaver (cleaving RNA with a NVB moitl), a cleaver (cleaving RNA with a YGY moitl). The CD20-targetting nucleic acid is used to cleaver RNA of CD20 in the presence of a divalent cation that is preferably Mg^2+.

The coll and treat a patient having a condition associated with the level cor CCC treat lymphom a luckaemia, the CD20 targetting nucleic acid may be used to the call and treat a patient having a condition associated with the level cor CCC treat lymphom a luckaemia, becall lymphoma, luckaemia, and inflammatory arthrogathy. The NOGO targetting nucleic acid is used to cleave RNA of the NOGO gene in the cucleic acid may be contacted with a cell lymphomy. The NOGO created with a cell and treat a patient having a condition associated with the level of concern and inflammatory arthrogathy. The NOGO created with a cell to reduce NOGO activity of the nucleic acid may be contacted with a cell to reduce NOGO activity of the cucleic acid may be contacted with a cell to reduce NOGO activity of the cucleic acid may be contacted with a cell to reduce on a nore control of a disease, disease, muscular accident (CNGO, the treatment may further comprise the use of cone or more theraptes. In particular, the NOGO-targetting nucleic acid may be contacted with a cell to reduce NOGO activity of the cuch central nervous system (NNS) injury and creatal sclerosis (MS). Chemotherapy-induced neuropathy, and/cor other neurodegeneral in which respond to the modulation of NOGO expression. The
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Best Local Similarity
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Search completed: December 13, 2005, 13:34:14 Job time : 370.5 sece

09-FEB-2001; 2001WO-US004273.

40200159103-A2

Synthetic.

16-AUG-2001

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Pasha, A.Q. and Ahsan, A.
Method of detecting predisposition to high altitude pulmonary edema
Patent: WO 2006047540-A 26-MAY-2005;
Council of Scientific and Industrial Research (IN)
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AX219959 | AR33530 | AR33530 | AR336775 | AR336775 | AR316755 | AR219922 | AR228622 | AR228922 | AR229910 | AR22010 
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noFe="Synthetic Oligonucleotide"
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CS101222
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AX219916 AX219918 AX421992 S
AX4315577 S
AX315598 AX219985 AX219985 AX219985 AX219985 AX219985 AX51865 AX51865 AX51865 AX51865 AX5111 S
AX219911 AX21993 AX519953 AX519953 AX519953 AX519953 AX519953 AX519953 AX519953
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                                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                              5883141 seqs, 28421725653 residues
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Listing first 45 summaries
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/organism="synthetic construct"
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                          Blatt, L., Mcswiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 01531013-A 5395 16-AUG-2001;
RIBOZYME PHARMACEUTIALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
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Method and reagent for the modulation and diagnosis of cd2.
nogo gene expression
Patent: WO 0159103-A 5358 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US)
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Patent: WO 0157206-A 1941 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Fattaey, Ali
Location/Qualifiers
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Thompson, J., Mcswiggen, J., Mckenzie, T., Ayers, D., Szymkowski, D.E. and Grupe, A. Mcthod and rangent for the inhibition of calcium activated chloride channel—1 (clca-1)
Patent: WO 0211674-A 3502 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US); Syntex (U.S.A.) LLC (US); Thompson, James (US)
Location/Qualifiers
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(US)
                                                                                                                                                                                    Query Match 69.2%; Score 16.6; DB 6; Length 37; Best Local Similarity 82.6%; Pred. No. 1.1e+04; Matches 19; Conservative 0; Mismatches 4; Indels
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McSwiggen, James (US); Chowrira, Bharat M. Location/Qualifiers
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82.6%; Pred. No. 1.1e+04;
iive 0; Mismatches 4;
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AX219924.1 GI:15547648
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                                                                                                              PAT 17-AUG-2003
                                                                                                                                                                                                                                                  Paveo,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J..
Paveo,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 13000 20-MAY-2003;
Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO
Ribozyme Docation/Qualifiers
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Unclassified.

(Mclassified.

Lobes 1 to 36)

Eckstein,F., Ludwig,J. and Beigelman,L.

Nucleic acid catalysts with endonuclease activity

Patent: US 6656731-A 597 02-DEC-2003;

Pax Planck Gesellschaft zur Forderung der Wissenschaften E.V. and Sirna Therapeutics; Munich;

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0; Mismatches 2; Indels
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89.5%; Pred. No. 2.6e+04;
iive 0; Mismatches 2;
                                                                                                         Sequence 13000 from patent US 6566127. AR335598
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AR436338
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Sequence 5427 from Patent WO0159103.
AX219985
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23
                 GGAGTGATGCCATGCACTA 20
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Best Local Similarity 89.5'
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Method and reagent for the inhibition of erg
Patent: WO 018124-A 3368 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 12979 20-MAY-2003,
Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, C
Location/Qualifiers
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                                                                                Score 16.2; DB 6; Length 37; Pred. No. 1.7e+04; 0; Mismatches 3; Indels
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
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Sequence 12979 from patent US 6566127.
AR335577.
AR335577.1 GI:33721385
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other sequences; artificial sequences.
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Sequence 3368 from Patent WO0188124.
AX425032
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/wol_type="unassigned RNA"
 /mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
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Best Local Similarity 85.73
Matches 18; Conservative
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Best Local Similarity 85.7
Matches 18; Conservative
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channel-1 (clca-1)
Patent: WO 0211674-A 3526 14-FEB-2002;
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Location/Qualifiers
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                                                                                          Blatt, L., Mcswiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0153103-A 5427 16-AUG-2001;
RIBOXYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Described and reagent for the modulation and diagnosis of cd20 and nogo gene expression
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
1. 37
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/mol Lype="unassigned RNA"
/db Zref="taxon:32630"
/noTe="Nucleic Acid"
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89.5%; Pred. No. 2.6e+04;
ive 0; Mismatches 2;
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="texon:32630"
/noTe="Nucleic Acid"
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                                                               other sequences; artificial sequences.
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AX228555
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    AX219985.1 GI:15547709
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AX223033
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Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1) Patent: WO 0211674-A 3492 14-FEB-2002; RIBOZYME PHARMACEUTICALS, INC. (US); Syntex (U.S.A.) LLC (US);
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Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)
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Fattaey, A.R., Jarvis, T., Mcswiggen, J., Booher, R.N. and Holman, P.S. Method and reagent for the inhibition of checkpoint kinase-1 (chk l) enzyme
19 enzyme
Patent: WO 0157206-A 1927 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Fattaey, Ali R. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thompson, J., Mcswiggen, J., Mckenzie, T., Ayers, D., Szymkowski, D.E.
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65.8%; Score 15.8; DB 6;
Best Local Similarity 89.5%; Pred. No. 2.6e+04;
Matches 17; Conservative 0; Mismatches 2;
                                                                                                                                                  1. .37
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                             ch 65.8%; Score 15.8; DB 6; Similarity 89.5%; Pred. No. 2.6e+04; 17; Conservative 0; Mismatches 2
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/mol_type="unassigned RNA"
/db xref="taxon:32630"
/noFe="Enzymatic Nucleic Acid"
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AX581654
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AX581688
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PAT 07-SEP-2001
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
patent: WO 0159103-A 5401 16-AUG-2001;
RIBOZYME HARMACEUTICALS, INC. (US); Blatt, Lawrence (US); McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
patent: WO 0159103-A 5394 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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                                                                                                      Length 37;
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Pred. No. 3.2e+04;
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/note="Nucleic Acid"
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/mol type="unassigned RNA"
/mol type="unassigned"
/noFe="Nucleic Acid"
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                                                                                           65.0%; Scor.
81.8%; Pred. No. 5...
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Sequence 5394 from Patent W00159103.
AX219952
AX219952.1 GI:15547676
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
patent: WO 0153103-A 5385 16-AUG-2001;
RIBOZYME HARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
     RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) Thompson, James (US) Location/Qualifiers
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Pred. No. 2.6e+04;
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/organism="synthetic construct"
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/nofe="Enzymatic Nucleic Acid"
                                                        1.37
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/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"
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Sequence 5385 from Patent WO0159103.
AX219943
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l Similarity 89.5%;
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PAT 17-AUG-2003

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FEATURES

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KEYWORDS SOURCE

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Unclassified.

1 (bases 1 to 36)
Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions
Method and reagent for the treatment of prowth factor receptor
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 14177 20-MAY-2003;
Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases I to 36)
Pavco, P., McKaiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Pavco, P., McKaiggen, T.A., Stinchcomb, D.T. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 656127-A 14200 20-MAY-2003;
Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO
Location/Qualifiers
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Pred. No. 4.9e+04;
0; Mismatches 3;
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1 (bases 1 to 36)
Eckstein,F., Ludwig,J. and Beigelman,L.
    AR336775 36 bp RNA Sequence 14177 from patent US 6566127. AR336775
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Sequence 825 from patent US 6656731.
AR436566.1 GI:40199650
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                                                           AR336775.1 GI:33722583
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Best Local Similarity 85.0%;
Matches 17; Conservative 0
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Best Local Similarity 85.0°
Matches 17; Conservative
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Unclassified.
1 (Dases 1 to 36)
1 (Dases 1 to 36)
Pavco, P., McSwigen, J.A., Stinchcomb, D.T. and Escobedo, J.
Rethod and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 12725 20-MAY-2003;
Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    Unknown.
Unclassified.
1 (bases 1.0.36)
1 (bases 1.0.36)
2 (bases 1.0.36)
Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 12711 20-MAY-2003;
Ribozyme Pharmactericals, Inc. and Chiron Corporation; Boulder, CO
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    Length 37;
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                                         4; Indels
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Query Match
65.0%; Score 15.6; DB 6;
Best Local Similarity 81.8%; Pred. No. 3.2e+04;
Matches 18; Conservative 0; Mismatches 4;
                                                                                                                                                                                                           36 bp RNA Sequence 12711 from patent US 6566127. AR335309.1 GI:33721117
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ACCESSION VERSION KEYWORDS

ORGANISM

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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
patent: WO 0159103-A 5504 16-AUG-2001;
RIBOZYME PHARMACEUTIAALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 5367 16-AUG-2001;
RIBOZYME PARAMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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Pred. No. 4.9e+04;
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Best Local Similarity 85.0%; Pred. No. 4.9e+04;
Matches 17; Conservative 0; Mismatches 3;
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/mol_type="unassigned RNA"
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/note="Nucleic Acid"
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/mol type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
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Sequence 5504 from Patent WO0159103.
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Sequence 5367 from Patent WO0159103.
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       /db_xref="taxon:32630"
/note="Nucleic Acid"
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Unclassified.
L (bases 1 to 36)
Eckstein. F., Ludwig, J. and Beigelman, L.
Nucleic acid catalysts with endonuclease activity
Nucleic acid catalysts with endonuclease activity
Max Planck Gesellschaft zur Forderung der Wissenschaften E.V. and
Sirna Therapeutics; Munich;
Nucleic acid catalysts with endonuclease activity
Patent: US 6656731-A 825 02-DEC-2003;
Max Planck Gesellschaft zur Forderung der Wissenschaften E.V. and
Sirna Therapeutics; Munich;
DEX;
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Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0153103-A 5364 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
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63.3%; Score 15.2; DB 6;
Best Local Similarity 85.0%; Pred. No. 4.9e+04;
Matches 17; Conservative 0; Mismatches 3;
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Sequence 1014 from patent US 6656731.
AR436755.
AR436755.1 GI:40199839
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Sequence 5364 from Patent W00159103.
AX219922
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/organism="unknown"
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AR436755
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AX219922
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PAT 18-JUN-2002

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Thompson, J., Mcswiggen, J., Mckenzie, T., Ayers, D., Szymkowski, D.E. and Grupe, A. Method and reagent for the inhibition of calcium activated chloride channel—1 (clca—1)
Patent: WO 0211674-A 3453 14-FEB-2002;
RIBOZYME PHARMACEUTCALS, INC. (US); Syntex (U.S.A.) LLC (US);
Thompson, James (US)
Location/Qualifiers
                                                                                                                                                                                     Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Mclaughlin, F.G. and Randi, A.M.
Randi, A.M.
Method and reagent for the inhibition of erg
Patent: WO 0188124-A 3288 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 63.3%; Score 15.2; DB 6; Length 37; Best Local Similarity 85.0%; Pred. No. 4.9e+04; Matches 17; Conservative 0; Mismatches 3; Indels
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Sequence 3453 from Patent WO0211674.
AXS81615.
AXS81615.1 GI:27653425
                    37 bp RN
Sequence 3288 from Patent WO0188124.
AX424952
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Sequence 5339 from Patent WO0159103.
AX219897.1 GI:15547621
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AX581615
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Patent: WO 0157206-A 1894 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Fattaey, Ali R. (US)
Location/Qualifiers
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Patent: WO 0157206-A 1917 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
Location/Qualifiers
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85.0%; Pred. No. 4.9e+04;
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Sequence 1894 from Patent WO0157206.
AX228522
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Sequence 1917 from Patent WO0157206.
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AX228545.1 GI:15557686
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 5553 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
Blatt, L., Mcswiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 5453 16-AUG-2001;
RIBOZYME HARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
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Sequence 5542 from Patent W00159103.
AX220100
AX220100.1 GI:15547824
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Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0153103-A 5352 16-AUG-2001;
RIBOXYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
                                                                                           Blatt, L., Mcswiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0153103-A 5339 16-AUG-2001;
RIBOTME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
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/db_xref="taxon:32630"
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Sequence 5453 from Patent W00159103.
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Sequence 5352 from Patent WO0159103.
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AX220011
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AX219910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blatt, L., Mcswiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 5562 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
ROSWiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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Patent: WO 0157206-A 1981 09-AUG-2001;
RIBOZYWE PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
Location/Qualifiers
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                                                                                                                                                      62.5%; Score 15; DB 6; Length 37; 78.3%; Pred. No. 6.1e+04; 1ive 0; Mismatches 5; Indels
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McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
                              1. 37
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db xref="texon:22630"
/note="Nucleic Acid"

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|mol type="unassigned RNA"
|db_xref="taxon:32630"

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Sequence 5562 from Patent WO0159103.
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AUTHORS
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                                             Gaps
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Patent: WO 0157206-A 1982 09-AUG-2001;
RIBOZYWE PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
Location/Qualifiers
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62.5%; Score 15; DB 6; Length 37; 78.3%; Pred. No. 6.1e+04;
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    .37
    forganism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"

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387902, 503486, 387702, 387807, 387902, 503486,

Sequence

Sequence Sequence Sequence Sequence

1313893, 1345869, 1360531, 1526049, 1529226,

92175, A 624295,

Sequence Sequence Sequence

Sequence

Sequence 1302115, Sequence 1313799, Sequence 1313893, Sequence 1345869,

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Run on:

Sequence:

Searched:

Database

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61.7%; Score 14.8; DB 8; Length 19; 77.8%; Pred. No. 4.1e+02; Live 2; Mismatches 2; Indels
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APPLICANT: KRYONOVA, Anattasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marball, William
APPLICANT: Scaringe, Stephen
ITTLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REPERENCE: 13499US
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
SPRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
US-11-101-244-387807

US-11-101-244-587902

US-11-083-784-387807

US-11-083-784-387807

US-11-083-784-387807

US-11-083-784-387807

US-11-083-784-387807

US-11-101-244-62255

US-11-101-244-131399

US-11-101-244-1313893

US-11-101-244-136589

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US-11-101-244-13693

US-11-083-784-62255

US-11-083-784-62295

US-11-083-784-133893

US-11-083-784-133893

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US-11-083-784-133893

US-11-083-784-1313893
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Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 253506, Application US/11101244; Publication No. US20050246794A1; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-11-101-244-253506
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Best Local Similarity
    RESULT 2
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    Matches
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Sequence 452572,
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Sequence 639666,
Sequence 940716,
Sequence 940758,
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Sequence 314817,
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                                                                                                                                                    December 13, 2005, 13:34:24 ; Search time 214.5 Seconds (without alignments) 41.830 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpna/USI1_NEW_PUB.seq3:*
                           GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Result

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Sequence 36, Application US/10508932

Sequence 36, Application US/10508932

Publication No. USZ0050260586A1

GENERAL INFORMATION:

APPLICANT: Weaver, David A.

APPLICANT: Weaver, David A.

APPLICANT: Weaver, Timothy G.

APPLICANT: Crawford, Erin L.

APPLICANT: Crawford, Erin L.

TITLE OF INVENTION: Method and Compositions for the Diagnosis and Treatment of Non-S.

TITLE OF INVENTION: Lung Cancer Using Gene Expression Profiles

FILE REPERENCE: 9060

CURRENT APPLICATION NUMBER: US/10/508,932

CURRENT FILING DATE: 2004-09-24

NUMBER OF SEQ ID NOS: 48

SEQ ID NOS: 48

SEQ ID NO 36

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 19;
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-318
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR PILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-11-14
PRIOR PLILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NOS: 1591911
SEQ ID NO 126494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 60.0%; Score 14.4; DB 9; Best Local Similarity 87.5%; Pred. No. 6.2e+02; Matches 14; Conservative 1; Mismatches 1;
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Pred. No. 6.3e+02;
0; Mismatches 6;
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Sequence 314817, Application US/11101244
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Rhvorova, Anaetasia
APPLICANT: Reyrolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
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Best Local Similarity 75.09
----hen 18; Conservative
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; ORGANISM: Homo sapiens
US-10-508-932-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-11-083-784-126494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 126494, Application US/11101244

Sequence 126494, Application US/11101244

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Responds, Angela
APPLICANT: Responds, Angela
APPLICANT: Marchall, William
APPLICANT: Marchall, William
APPLICANT: Scaringe, Stephen
ITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 2003-10-10

NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 126494
LENGTH: 19
          HAPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 1349908
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
FRICA APPLICATION NUMBER: US/10/714,333
FRICA FILING DATE: 2003-11-14
FRICA FILING DATE: 2003-010
FRICA PLING DATE: 2003-010
FRICA FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 25506
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.7%; Score 14.8; DB 9; 77.8%; Pred. No. 4.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
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Sequence 126494, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khyorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 TGCACAGCTGGGGAACAA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-11-083-784-253506
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US-11-101-244-126494
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rhyorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Respective, Devin
APPLICANT: Respective, Devin
APPLICANT: Respective, Devin
APPLICANT: Marshall, William
FILE REFERENCE: 13499US
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 452572
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 19;
            APPLICANT: Scaringe, Stephen:
TITLE OF INVENTION: Functional and Hyperfunctional siRNA FILE OF INVENTION: Functional and Hyperfunctional siRNA FILE OF INVENTION NUMBER: US/11/101,244
CURRENT APPLICATION NUMBER: US/502,050
PRIOR PILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2002-11-14
NUMBER OF SILING DATE: 2002-11-14
NUMBER OF SILING DATE: 2002-11-14
NUMBER OF SILING DATE: 2002-11-14
SOFTWARE: Proprietary
SOFTWARE: Proprietary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 57.5%; Score 13.8; DB 8; Best Local Similarity 82.4%; Pred. No. 1.2e+03; Matches 14; Conservative 1; Mismatches 2;
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APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 GCACAGCTGGGGAACAA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: RNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                   TYPE: RNA
CORGANISM: Homo sapiens
US-11-101-244-253501
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Best Local Similarity
Matches 14; Conserva
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US-11-101-244-452581
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TITLE OF INVENTION: Functional and Hyperfunctional siRNA FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-11-14
SUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FIRE REPREDENCE: 13499US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 14.2; DB 9;
Pred. No. 7.6e+02;
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CURRENT PILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-11-14
PRIOR PLIING DATE: 2003-09-10
PRIOR PLIING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
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Sequence 253501. Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khovorova, Anastasia
APPLICANT: Khovorova, Anastasia
APPLICANT: Leake, Devin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 314817, Application US/11083784 Publication No. US20050245475A1 GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GCACAGCUCAGGAACUAGA 19
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Best Local Similarity 78.9%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              59.2%;
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 78.9
Matches 15; Conservative
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US-11-083-784-314817
                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-11-101-244-314817
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LENGTH: 19
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Gaps

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57.5%; Score 13.8; DB 8; Length 19; 82.4%; Pred. No. 1.2e+03;
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US-11-101-244-987947
; Sequence 987947, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Charmacon, Inc.
; APPLICANT: Reynolds, Angela
; APPLICANT: Respect Devin
; APPLICANT: Marehall, William
; APPLICANT: Marehall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Khorova, Anascasia
APPLICANT: Khorova, Anascasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Dovin
APPLICANT: Leake, Devin
APPLICANT: Bearbail, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: PROPRIETE 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
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TITLE OF INVENTION: Functional and Hyperfunctional siRNA
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                      FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR PELICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEO ID NOS: 1591911
SOFTWARE: Proprietary
SOFTWARE: 10 NO 940716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-11-101-244-940758
; Sequence 940758, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 ACAGCTGGGGAACAAGA 22
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| AAAGCUGAGGAACAAGA 18
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Best Local Similarity 82.4
Matches 14; Conservative
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Best Local Similarity 82.4;
Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-11-101-244-940758
                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-11-101-244-940716
                                                                                                                                                                                                                                                                                                 TYPE: RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                        Score 13.8; DB 8; Length 19;
Pred. No. 1.2e+03;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 639666, Application US/11101244

publication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Respondes, Stephen
TILLE REFERENCE: 1349908
CURRENT FILING DATE: 2005-04-07
PRIOR PLICATION NUMBER: 60/502,050
PRIOR PLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2003-09-10
PRIOR REPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
SOFTWARE: Proprietary
SEC ID NO 639666
LENGTH: 19
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR PELICATION NUMBER: 60/502,050
PRIOR PELICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 452581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 940716, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INPORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
( ; APPLICANT: Scaringe, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 TGCACAGCTGGGGAACA 19
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Best Local Similarity 82.4%;
Matches 14; Conservative
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Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-11-101-244-639666
                                                                                                                                                                                                                                                                                                                                ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-452581
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; Publication No. US20050245475A1
; GENERAL INFORMATION:
    APPLICANT: Dharmacon, Inc.
    APPLICANT: Revnoids, Ansetasia
    APPLICANT: Revnoids, Ansetasia
    APPLICANT: Revnoids, Ansetasia
    APPLICANT: Leake Devin
    APPLICANT: Leake Devin
    APPLICANT: Scaringe, Stephen
    TITLE OF INVENTION: Functional and Hyperfunctional siRNA
    FILE REFERENCE: 1349908:
    CURRENT APPLICATION NUMBER: US/11/083,784
    CURRENT FILING DATE: 2005-03-18
    PRIOR APPLICATION NUMBER: 60/502,050
    PRIOR PLING DATE: 2000-11-14
    PRIOR APPLICATION NUMBER: 60/426,137
    PRIOR FILING DATE: 2002-11-14
    PRIOR RILING DATE: 2002-11-14
    PRIOR APPLICATION NUMBER: 60/426,137
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82.4%; Pred. No. 1.2e+03;
ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 19;
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TITLE OF INVENTION: Functional and Hyperfunctional siRNA
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82.4%; Pred. No. 1.2e+03;
tive 1; Mismatches 2;
                       FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT ETLING DATE: 2005-03-18
PRIOR PLINGEDATE: 2005-11-14
PRIOR PLINGEDATE: 2003-11-14
PRIOR PLINGEDATE: 2003-09-10
PRIOR PLINGEDATE: 2003-09-10
PRIOR PLINGEDATE: 2003-09-10
PRIOR PLINGEDATE: 2003-11-14
PRIOR PLINGEDATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
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| Sequence 639666, Application US/11083784
| Publication No. US20050245475A1
| GENERAL INFORMATION:
| APPLICANT: Dharmacon, Inc.
| APPLICANT: Rivorova, Anastasia
| APPLICANT: Reynolds, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 GCACAGCTGGGGAACAA 20
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Best Local Similarity 82...
Local Similarity 82...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 82.4'
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-452572
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sequence 253501, Application US/11083784
sublication No. U320050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.,
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Marball, William
APPLICANT: Marball, William
APPLICANT: Marball, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR PLILING DATE: 2003-09-10
PRIOR PLILING DATE: 2003-09-10
PRIOR PLILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 253501
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Pred. No. 1.2e+03;
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                       CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
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APPLICANT: Khvorova, Anaetasia
APPLICANT: Reynolda, Angela
Leake, Devin
APPLICANT: Marehall, William
APPLICANT: Scaringe, Stephen
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Best Local Similarity 82.4%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                        ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-987947
     FILE REFERENCE: 13499US
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US-11-083-784-253501
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US-11-083-784-940716
i Sequence 940716, Application US/11083784
i Sequence 940716, Application US/11083784
i Sequence 940716, Application US/11083784
i GENERAL INFORMATION:
i APPLICANT: Khyorova, Ansetasia
APPLICANT: Khyorova, Ansetasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: More Searinge, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 1349908
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
SHOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: POPPICATY
SEQ ID NO 940716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 57.5%; Score 13.8; DB 9; Length 19; Best Local Similarity 82.4%; Pred. No. 1.2e+03; Matches 14; Conservative 1; Mismatches 2; Indels
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT PILNO BATE: 2005-03-18
FRIOR PILING DATE: 2003-11-14
FRIOR PILING DATE: 2003-11-14
FRIOR FILING DATE: 2003-11-14
FRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
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US-11-083-784-940716
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-11-083-784-639666
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; Publication No. US20050245475A1
; GENERAL INFORMATION:
   APPLICANT: Dharmacon, Inc.
; APPLICANT: Reynolds, Angela
   APPLICANT: Reynolds, Angela
   APPLICANT: Reznolds, Angela
   APPLICANT: Reznolds, Angela
   APPLICANT: Reznolds, Angela
   APPLICANT: Marchall, William
   APPLICANT: Marchall, William
   APPLICANT: Marchall, William
   APPLICANT: Marchall, William
   APPLICANT: Bcaringe, Stephen
   TITLE OF INVENTION: Functional and Hyperfunctional siRNA
   FILE REFERENCE: 13499US
   CURRENT APPLICATION NUMBER: US/11/083, 784
   CURRENT PILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/50,050
   PRIOR FILING DATE: 2003-11-14
; PRIOR PLLING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEG ID NOS: 1591911
; SOFTWARE: Proprietary
   LENGTH: 19
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                                              APPLICANT: Leafe, Devin
APPLICANT: Leafe, Devin
APPLICANT: Acashing, Stephon
APPLICANT: Scaringe, Stephon
TITLE OF INVENTON: Functional and Hyperfunctional siRNA
FILE REPERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR PPLICATION NUMBER: US/10/714,333
PRIOR PILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-10-10
PRIOR FILING DATE: 2003-10-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: PROPIECATION
SEQ ID NO 940758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 57.5%; Score 13.8; DB 9; Best Local Similarity 82.4%; Pred. No. 1.2e+03; Matches 14; Conservative 1; Mismatches 2;
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Khvorova, Anastasia
Reynolds, Angela
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Best Local Similarity 82.4<sup>†</sup>
Matches 14; Conservative
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US-11-083-784-987947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-11-083-784-940758
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US-11-083-784-987947
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RESULT 22 US-10-770-726-10883/c

Sequence 940758, Application US/11083784 Publication No. US20050245475A1 GENERAL INFORMATION:

US-11-083-784-940758

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Pred. No. 1.7e+03;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 387992, Application US/11101244
; Sequence 387992, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Whyorous, Inc.; APPLICANT: Khyorous, Ansetasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Beake, Devin
; APPLICANT: Beake, Devin
; APPLICANT: Beake, Devin
; APPLICANT: Scaringe, Stephen
; TITLE DG INVENTION: Functional and Hyperfunctional siRNA
; TITLE REFERENCE: 1149918
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; LENGTH. 10 D 387902
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 13.4; DB 8; Length 19;
Pred. No. 1.7e+03;
1; Mismatches 1; Indels
                 APPLICANT: Scatinge, Stephen
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
FILE REPERENCE: 13499US
FILE REPERENCE: 1349US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR PLILING DATE: 2005-010
PRIOR PLILING DATE: 2002-11-14
FRIOR PLILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 387807
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Publication No. US20050246/94A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Revorova, Angela
APPLICANT: Revolubs, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
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Best Local Similarity 86.7%;
Matches 13; Conservative
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Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-387902
                                                                                                                                                                                                                                                                                                                                   TYPE: RNA
CORGANISM: Homo sapiens
US-11-101-244-387807
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US-11-101-244-503486
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                                                                                            APPLICANT: Brown, Eugene
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 56.7%; Score 13.6; DB 6; Length 21; Best Local Similarity 80.0%; Pred. No. 1.4e+03; Matches 16; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 387702, Application US/11101244
; Publication No. US20050346794A1
; GENERAL INFORMATION:
; APPLICANT: Inharmacon, Inc.;
; APPLICANT: Rhyorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REPERENCE: 13499US
CURRENT APPLICATION NUMBER: 60/502.050
PRIOR PLING DATE: 2005-09-10
PRIOR PLING DATE: 2005-09-10
PRIOR PLING DATE: 2002-11-14
; SOFTWARE: Proprietary
; SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
Sequence 10883, Application US/10770726
Publication No. US20050266409A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 TGCACAGCTGGGGAACAAGA 22
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; ORGANISM: Homo sapiens
US-10-770-726-10883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-11-101-244-387702
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                                                                               APPLICANT: Wyeth
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Score 13.4; DB 9; Length 19;
pred. No. 1.7e+03;
1; Mismatches 1; Indels
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; Publication Wo. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Datarmacon, Inc.
; APPLICANT: Reynolds, Ansetasia
; APPLICANT: Reynolds, Ansetasia
; APPLICANT: Responds, Ansetasia
; APPLICANT: Leake, Devin
; APPLICANT: Leake, Devin
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; TITLE OF INVENTION: Functional and Hyperfunctional
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional
; PRICANT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-10-14
; PRIOR FILING DATE: 2003-11-14
; RICAN APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
               APPLICANT: Scatinge, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
TITLE REPERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR FILING DATE: 2005-10-14
PRIOR FILING DATE: 2003-10-14
PRIOR PLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PLILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO3 387807
LENGTH: 19
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US-11-083-784-503486
; Sequence 503486, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
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Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-387902
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-11-083-784-387807
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 13.4; DB 8; Length 19;
Pred. No. 1.7e+03;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 387702, Application US/11083784
; Bublication No. US202050245475A1
; Bublication No. US202050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.;
; APPLICANT: Reynolds, Angela
; APPLICANT: Responds, Angela
; APPLICANT: Marchall, William
; APPLICANT: Marchall, William
; APPLICANT: Marchall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; TILE OF INVENTION: Functional and Hyperfunctional
; FILE REFERENCE: 13499U
; CURRENT APPLICATION NUMBER: US/11/043,784
CURRENT FILING DATE: 2005-010
; PRIOR PLICATION NUMBER: 60/502,050
; PRIOR PLICATION NUMBER: 60/502,050
; PRIOR PLICATION NUMBER: 60/426,137
; PRIOR PLILNG DATE: 2003-09-10
; PRIOR PLILNG DATE: 2002-11-14
; PRIOR PLILNG DATE: 2002-11-14
; SOFTWARE: Proprietary
; SEQ ID NO 387702
LENGITH: 19
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 1499 9US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
FRIOR APPLICATION NUMBER: 60/502,050
FRIOR APPLICATION NUMBER: 60/426,137
FRIOR APPLICATION NUMBER: 60/426,137
FRIOR PILING DATE: 2002-011-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
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; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Characon, Inc.
; APPLICANT: Khovorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
                                                                                                                                                                                                                                                                                                                                                                                                                                             55.8%;
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Best Local Similarity 80.09
Matches 12; Conservative
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US-11-083-784-387702
                                                                                                                                                                                                                                                                                                                                      TYPE: RNA
CRGANISM: Homo sapiens
US-11-101-244-503486
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                             APPLICANT: Leake, Devin
APPLICANT: Acring.
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT PILING DATE: 2005-04-07
PRIOR PILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 624295
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Khorova, Anaetasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13490US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1302115, Application US/11101244; Publication No. US20050246794A1; GENERAL INFORMATION:
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SOFTWARE: Proprietary
SEQ ID NO 1302115
LENGTH: 19
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Best Local Similarity 72.2
Matches 13; Conservative
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Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Homo sapiens
US-11-101-244-624295
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US-11-101-244-1302115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.8%; Score 13.4; DB 9; Length 19; 80.0%; Pred. No. 1.7e+03; Live 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence 92175, Application US/11101244
publication No. US200S0246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Maraball, William
APPLICANT: Maraball, William
APPLICANT: Maraball, William
APPLICANT: Scaringe, Stephen
TITLE OF INSWITON: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SSCFTWARE: Proprietary
LENGTH: 19
         APPLICANT: hasynana, hasynana, hasynana, hasynana, hashall, william, appLICANT: marshall, william, appLICANT: marshall, william, appLICANT: Scaringe, Stephen TILLE APPLICANT: Scaringe, Stephen TILLE OF INVESTION: Functional and Hyperfunctional siRNA FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/50,50
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PLIING DATE: 2003-03-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 503486
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0, Mismatches
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UGCACAGCUGGAGAA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 TGCACAGCTGGGGAA 17
  Angela
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Best Local Similarity 83.33
Matches 15; Conservative
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Best Local Similarity 80.0
Matches 12; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-11-083-784-503486
Reynolds,
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US-11-101-244-92175/c
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US-11-101-244-624295
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Sequence 1526049, Application US/11101244, Publication No. US20050246794A1, GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Rivorova, Anastasia, APPLICANT: Reynolds, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 CACAGCUGGUGAGGAAGA 19
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      Reynolds, Angela
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US-11-101-244-1360531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-11-101-244-1345869
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US-11-101-244-1360531
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Pred. No. 2.2e+03;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 13.2; DB 8; Length 19;
Pred. No. 2.2e+03;
2; Mismatches 3; Indels
                   APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marshall, Welliam
APPLICANT: Marshall, Welliam
APPLICANT: Marshall, Welliam
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFREENCE: 134990US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SGOTWARE: Proprietary
SEQ ID NOS: 1591911
SGOTWARE: PLODRICATION
SEQ ID NOS: 1591911
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Publication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Respect Devin
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Leake, Devin
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR PELICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 60/426,137
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Khvorova, Anastasia
Reynolds, Angela
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APPLICANT: Khvorova, Anastasia
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Best Local Similarity 72.2%;
Matches 13; Conservative
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Best Local Similarity 72.2%;
Matches 13; Conservative
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US-11-101-244-1313799
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US-11-101-244-1313893
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APPLICANT: Khvorova, Anastasia
APPLICANT: Reyrolds, Angela
APPLICANT: Beake, Devin
APPLICANT: Marchall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 1360531
LENGTH: 19
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: 08/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SCPTWARE: Proprietary
SEQ ID NOS: 1591911
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GENERAL IPPORMATION:
APPLICANT: Dharmacon, Inc.
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Marshall, William
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APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PLING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1526049
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Publication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Characon, Inc.
APPLICANT: Rivorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
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CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
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; Sequence 92175, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Rivorova, Anastasia
; APPLICANT: Reynolds, Angela
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2 AAAGUUGGAGAACAAGAC 19
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Best Local Similarity 72.2 Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA
CORGANISM: Homo sapiens
US-11-101-244-1526049
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US-11-101-244-1529226
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APPLICANT: SCATINGS, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 1349904
FILE REFERENCE: 1349904
CURRENT FILING DATE: 2005-03-18
FRIOR PILING DATE: 2003-11-14
FRIOR PLING DATE: 2003-19-10
FRIOR PLING DATE: 2003-19-10
FRIOR PLING DATE: 2003-19-10
FRIOR PLING DATE: 2003-19-10
FRIOR PLING DATE: 2002-11-14
FRIOR FLING DATE: 2002-11-14
FRIOR PLING DATE: 2003-11-14
FRIOR PLING DATE: 2003-10-10
FRIOR APPLICATION NUMBER: 60/426/137
FRIOR PLING DATE: 2003-11-14
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